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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                              OM protein - protein search, using sw model
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Pebruary 16, 2006, 01:14:10 ; Search time 132 Seconds
(without alignments)
1115.090 Million cell updates/sec Run on:

US-10-733-782-1 1678 Perfect score:

1 AIDENKQKALAAALGQIEKQ........AKEIEKKVRELLLSNPNSTP 335 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2443163 seqs, 439378781 residues Searched:

2443163 Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB

seq length: 0 seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:* A_Geneseq_21:* 4.0.07.80 Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Adr16428 E. coli R	Adr16432 E. coli w	Abul5395 Protein e	Aay68827 Amino aci	-	Adq87824 E. coli r	œ.	ы.	Ami	Adr16430 E. coli R	Aaw64213 New minsh	Aay68828 Amino aci	Adq87823 E. coli r	Adq87826 E. coli r	Aaw64215 Hyperreco	Aaw64214 Hyperreco	Aaw64217 Hyperreco	Aaw64218 Hyperreco		Adq87827 E. coli r	Aay68830 Amino aci	Adq87825 E. coli r	Aaw64216 Hyperreco	Abu48024 Protein e
SUMMARIES	ID	ADR16428	ADR16432	ABU15395	AAY68827	AAY68829	ADQ87824	ADQ87822	ADQ87821	AAY68831	ADR16430	AAW64213	AAY68828	ADQ87823	ADQ87826	AAW64215	AAW64214	AAW64217	AAW64218	AAY68832	ADQ87827	AAY68830	ADQ87825	AAW64216	ABU48024
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a	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	6.66	99.8	99.8	99.7	99.7	99.5	99.4	99.5	99.0	99.0	98.9	98.9	98.9	98.9	97.9	97.8
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ABU31601 ABO63433 ABU27708	ABM67793 ABU50600 ABU40669 ADP05150	ABU4971 ABU49151 ABU39491	ABU30311 ABO72381 ABU38581	ADA36276 ABU40018 ABU41878	ADL05025 ABU35468 ABU33125 AEB39711
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25 26 27	30 30 31 30 31	33 34 34	3 3 5 8 5 8 5 8 5 8 5 8 5 8 5 8 5 8 5 8	36 4 4 10 10 10	4 4 4 4 2 6 4 2

ALIGNMENTS

RecA; DNA binding protein; seDNA binding protein; SSB; DNA strand exchange reaction; site-specific cleavage; mutant; mutein. ADR16428 standard; protein; 335 AA. E. coli RecA mutant protein #1. (first entry) Escherichia coli. US2004157248-A1. 04-NOV-2004 12-AUG-2004. ADR16428; ADR16428

11-DEC-2003; 2003US-00733782. 12-DEC-2002; 2002US-0432758P.

(COXM/) COX M M. (LUSE/) LUSETTI S L. (EGGL/) EGGLER A L. (HARU/) HARUTA N.

Haruta N; Eggler AL, Cox MM, Lusetti SL,

WPI; 2004-580265/56. N-PSDB; ADR16429 New RecA mutant proteins comprising a single mutation or a double mutation, useful for catalyzing homologous DNA pairing and DNA strand exchange reactions in an in vitro or in vivo environment.

Claim 2; SEQ ID NO 1; 34pp; English.

The invention relates to an isolated RecA mutant protein, where the protein is either a single mutant RecA protein comprising a deletion of amino acid residues from the carboxyl terminus, or a double mutant RecA protein comprising a deletion of amino acid residues from the carboxyl terminus and an amino acid change from a glutamate to a basic amino acid. The invention also relates to a polynucleoride sequence that encodes the RecA mutant protein, a method of catalysing an in vitro homologous DNA pairing and DNA strand exchange reactions comprising providing an amount

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a cell comprising aupplying to the cell an amount of the RecA mutant contributed and cell an amount of the RecA mutant protein comprises an enhanced capacity to displace a DNA binding protein compared to wild-type RecA. The DNA binding protein is from Escherichia coll (SSB).

C talso comprises enhanced binding protein from Escherichia coll (SSB).

C traction as compared to wild-type RecA. The composition and methods are useful for catalysing homologous DNA pairing and DNA strand exchange creactions in an in vitro or in vivo environment. These may be used in promoting in vitro alterations of genes to permit the rapid construction of desired gene mutants for industrial and pharmaceutical purposes. The cutant proteins may also be used in targeting the site-specific classage of small and large DNAs, or as a basis for the design and construction of tiny electronic circuits based on DNA. This sequence represents a RecA
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of the RecA mutant protein and a method of increasing recombination efficiency of homologous DNA pairing and DNA strand exchange reactions in
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DNA strand exchange reaction; site-specific cleavage.
                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1678; DB 8;
100.0%; Pred. No. 5.7e-155;
iive 0; Mismatches 0;
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Matches 335; Conservative
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The invention relates to an isolated RecA mutant protein, where the protein is either a single mutant RecA protein comprising a deletion of amino acid residues from the carboxyl terminus, or a double mutant RecA protein comprising a deletion of amino acid residues from the carboxyl terminus and an amino acid change from a glutamate to a basic amino acid. The invention also relates to a polynucleotide sequence that encodes the RecA mutant protein, a method of catalysing an in vitro homologous DNA pairing and DNA strand exchange reactions comprising providing an amount of the RecA mutant protein and a method of increasing recombination of the RecA mutant protein and a method of increasing recombination of the RecA mutant protein as comprises an enhanced capacity to comprising supplying to the cell an amount of the RecA mutant protein as comprises an enhanced capacity to displace a DNA binding protein is the ssDNA binding protein from Esperature comprises enhanced binding to DNA strand exchange reaction as comprises enhanced binding to DNA during and DNA strand exchange consection is the ssDNA binding protein from Esperature and methods are reactions in an in vitro alld-type RecA. The composition and methods are useful for catalysing homologous DNA pairing and DNA strand exchange consections in an in vitro alterations of genes to permit the rapid construction of desired gene mutants for industrial and pharmaceutical purposes. The mutant proteins may also be used in transquering the site-specific cleavage of small and large DNAs, or as a basis for the design and construction of tiny electronic circuits based on DNA. This sequence represents the wild-type RecA protein of the invention.
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                                                                                                                                          New RecA mutant proteins comprising a single mutation or a double mutation, useful for catalyzing homologous DNA pairing and DNA strand exchange reactions in an in vitro or in vivo environment.
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Pred. No. 6.2e-155;
; Mismatches 0;
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Best Local Similarity 100.
Matches 335; Conservative
                                                             Lusetti SL,
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                  HARUTA
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                  (HARU/)
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ABU15395;

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WPI; 2003-029926/02
             Escherichia coli.
                                                N-PSDB; ACA19265.
                                                                                                                     Sequence 353 AA;
                 WO200277183-A2.
   19-JUN-2003
                    03-OCT-2002
                                         Wang L,
Wall D,
                                      (ELIT-)
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Zamudio C, Trawick JD,

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recA; hyperrecombinogenic variant; male gamete; female gamete; heat tolerance; ethanol production; ethanol tolerance; metabolite; taxol; cyclosporin A; erythromycin; meiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents the recA protein. The wild type recA protein was used to produce hyperrecombinogenic variants (see AAV68828-32), using the method of the invention. The specification describes a method for producing a library of diverse multicellular organisms using pools of male and female gameres. At least one of the male pool or female pools comprises a number of different gametes derived from different strains of a species or of a different species. The viable organisms produced from the fertilized gametes are repeatedly crossed to produce a
                                                                                                             61 IVEIYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSOPD
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                                     2 AIDENKOKALAAALGQIEKOFGKGSIMRLGEDRSMDVETISTGSLSIDIALGAGGLPMGR
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Bass S,
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Krebber CM,
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Castle LA, Kre
Affholter JA;
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ten PA, Subramanian V,
T, Huisman G, Yuan L,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the foll antiennes sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated or list fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway or that has an activity against a biological pathway or equired for proliferation, or that inhibits proliferation; (8) identifying a gene required for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound activity; (11) a compliant or the strains is present in a culture or collection of the which each of the strains is present in a culture or collection of the which each of the strains is present in a culture or collection of proliferation of an organism. The antisense nucleic acids are useful for dentifying proteins or sereains for homologous nucleic acids required for the displace and acids required for formal and accide and acids required for formal and accide and acids required for formal accided and activity of the accenning to homologous nucleic acids required for accided and activity accenning the candidate molecules for rational
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to an isolated nucleic acid comprising any one of
                                                                                                                               Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antisense nucleic acids, useful for identifying proteins or s
for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
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Forsyth RA,
                                                                           Protein encoded by Prokaryotic essential gene #922.
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 25; SEQ ID NO 43319; 1766pp; English.
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Carr GJ,
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25-0CT-2001; 2001US-0342923P.
08-PEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                        21-MAR-2002; 2002WO-US009107.
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                    (first entry)
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J; Zhang Y;

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2000-182446/16.

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            property. The methods can be used to evolve cells to acquire a desired property such as heat tolerance, ethanol production or tolerance, acid, improved production and maintenance of enzyme cofactors or NAD(P) H and improved glucose transport. The desired property may be expression of a protein or primary or secondary metabolite. Alternatively the desired property is secretion of a protein or secondary metabolite, chosen from taxol, cyclosporin A and erythromycin. The desired property may be a capacity for meiosis or compatibility to form a heterokaryon with another
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               recA; hyperrecombinogenic variant; male gamete; female gamete; heat tolerance; ethanol production; ethanol tolerance; metabolite; taxol; cyclosporin A; erythromycin; meiosis.
                                                                                                                                                                                                                                                                                                                     61 IVEIYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSQPD 120
                                                                                                                                                                                                                                                                                                                                         240
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organisms, which are selected for a desired trait
                                                                                                                                                                                                                                 Gaps
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, Bass S, Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of a hyperrecombinogenic recA protein clone 4.
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                                                                                                                                                                                                   Length 358;
                                                                                                                                                                                                                              Indels
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Castle LA, Krebber CM,
, Affholter JA;
                                                                                                                                                                                               / Match 100.0%; Score 1678; DB 3;
Local Similarity 100.0%; Pred. No. 6.3e-155;
Nes 335; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY68829 standard; protein; 358
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Patten PA, Subramanian V,
Cox T, Huisman G, Yuan L,
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The present sequence represents a hyperrecombinogenic rech protein. The wild type rech protein (AAY68827) was used to produce hyperrecombinogenic wild type rech protein (AAY68827) was used to produce hyperrecombinogenic variants, using the method of the invention. The specification describes camethod for producing a library of diverse multicellular organisms using pools of male and female gametes. At least one of the male pool or female pools of male and female gametes at least one of the male pool or female pools of strains of a species or of a different gametes derived from different consists. The viable organisms produced from the fertilized gametes are repeatedly crossed to produce a library of diverse organisms, which are selected for a desired trait or property. The methods can be used to evolve cells to acquire a desired comproved production and maintenance of enzyme cofactors or NAD(P)H and improved glucose transport. The desired production not a protein or secondary metabolite. Alternatively the desired property is secretion of a protein or secondary metabolite, chosen from the capacity for meiosis or compatibility to form a heterokaryon with another
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1678; DB 3; Length 358; 100.0%; Pred. No. 6.3e-155; ive 0; Mismatches 0; Indels 0.
                                              Evolution of whole cells and organism by iterative cycles of recombination and selection and screening for acquisition of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    335
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                                                                                                                         Example 1; Fig 13; 197pp; English.
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Best Local Similarity
               N-PSDB; AAZ60611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 358 AA;
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Tobin M;

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09-FEB-2004; 2004AU-00200501.
                09-FEB-2004; 2004AU-00200501.
                    (MAXY-) MAXYGEN INC
  Escherichia coli,
     AU2004200501-A1.
         04-MAR-2004
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The invention relates to a method of evolving cells to acquire a desired protoplasts of different cells, fusing the protoplasts of protoplasts from protoplasts of com hybrid protoplasts from protoplasts from the companies, includating protoplasts from protoplasts recombine to form hybrid protoplasts in which genomes from protoplasts recombine to form additional hybrid genomes and incubating additional hybrid protoplasts for producing additional hybrid protoplasts for genomes from protoplasts recombine to form additional hybrid genomes and incubating protoplasts for producing additional hybrid protoplasts for producing additional hybrid protoplasts for genomes and different producing protoplasts for genomes and a pool of female gametes or different gametes derived from different strains of a species or different gametes derived from different strains of a species or different gametes derived from different strains of a species or different gametes derived from different strains of a species or grow into reproductively viable centured property. The methods are useful for evolving cells to organisms, repeatedly crossing the reproductively viable organisms to desired property is methodicity or forman centured property. The method and maintenance of enzyme coffactors, improved production and maintenance of enzyme coffactors, improved production and maintenance of enzyme coffactors, improved production and maintenance of enzyme team, coffactors, improved production and maintenance of enzyme coffactors, deficient by the method is also useful for predicting efficacy of a drug in treating viral o
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                                                                                                                                                                                                                                                                                                                     Evolving cells to acquire a desired property, by forming protoplasts different cells, fusing protoplasts to form hybrid protoplasts (HP), producing regenerated cells, forming additional HP and producing additional regenerated cells.
         Ness JE, Tobii
Subramanian V;
         Patten PA,
Krebber CM,
Castle LA, Patter
Zhang Y, Krebber
Del Cardayre S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 13; 196pp; English.
Bass S, (uisman G,
Yuan L, Cox T, Bass S,
Affholter JA, Huisman G,
Minshull J, Stemmer WPC,
                                                                                                                                                                               WPI; 2004-507924/49.
N-PSDB; ADQ87817.
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Sequence 358 AA;

ö Query Match 100.0%; Score 1678; DB 8; Length 358; Best Local Similarity 100.0%; Pred. No. 6.3e-155; Matches 335; Conservative 0; Mismatches 0; Indels 0

60 99 AIDENKQKALAAALGQIEKQFGKGSIMRLGEDRSMDVETISTGSLSLDIALGAGGLPMGR 1 AIDENKOKALAAALGOIEKOFGKGSIMRLGEDRSMDVETISTGSLSLDIALGAGGLPMGR

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61 IVEIYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSQPD 120

180 186 240 246 300 RecA; protoplast formation; gamete; heat tolerance; ethanol production; ethanol tolerance; enzyme cofactor; NAD(P)H; glucose transport; meiosis; heterokaryon; taxol; cyclosporin A; erythromycin; viral infection; Evolving cells to acquire a desired property, by forming protoplasts of different cells, fushing protoplasts to form hybrid protoplasts (HP), producing regenerated cells, forming additional HP and producing additional regenerated cells. 127 TGEQALEICDALARSGAVDVIVVDSVAALTPKAEIEGEIGDSHWGLAARMASQAMRKLAG 187 NLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKPYASVRLDIRRIGAVKEGENVVGS ETRVKVVKNK1AAPFKQAEFQ1LYGEG1NFYGELVDLGVKEKL1EKAGAWYSYKGEK1GO 181 NLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLDIRRIGAVKEGENVVGS Tobin M; plant genome shuffling; micropore manipulation; reiterative pooling Ness JE, Tobir Subramanian V; Castle LA, Patten PA, Zhang Y, Krebber CM, Del Cardayre S; GKANATAWLKDNPETAKEIEKKVRELLLSNPNSTP 335 Disclosure, Fig 13; 196pp; English. ADQ87822 standard; protein; 358 AA E. coli recA protein clone #1. 09-FEB-2004; 2004AU-00200501. 09-FEB-2004; 2004AU-00200501 (first entry) Yuan L, Cox 1, Affholter JA, Huisman G, Cox T, Baber (MAXY-) MAXYGEN INC. 2004-507924/49. Escherichia coli. N-PSDB; ADQ87815 AU2004200501-A1. 09-SEP-2004 04-MAR-2004. ADQ87822; 241 247 301 307 ADQ87822 8 셤 ò 셤 ઠે 셤 ò

The invention relates to a method of evolving cells to acquire a desired protoplasts to forming protoplasts of different cells, fushing the protoplasts to form hybrid protoplasts. Incubating the hybrid protoplasts to produce regenerated cells, repeatedly forming protoplasts from regenerated cells, fusing protoplasts to form hybrid protoplasts in which sonomes from protoplasts recombine to form additional hybrid genomes and incubating additional hybrid protoplasts for producing additional regenerated cells. The invention also relates to a method of producing a library of diverse multicellular organisms involving providing a pool of male gametes and a pool of female gametes, where one of the male pool or the female pool comprises several different sametes derived from different strains of a species or different species and the male gametes

certilise the female gametes, permitting at least a portion of the resulting fertilised gametes to grow into reproductively viable organisms to organisms, repeatedly crossing the reproductively viable organisms to produce a library of diverse organisms and selecting the library for a certification by a second result of production and maintenance of enzyme channol tolerance, improved production and maintenance of enzyme cofactors, improved production and maintenance of maryme cofactors, improved production and maintenance of MAD(P)H and improved glucose transport. The desired property is the secretion of a protein or secondary metabolite, the secretion of a protein or captualition of desired properties such as enhanced recombinogenicity, gene copy number or gene reductivity and capacity for expression and/or secretion of proteins or secondary metabolites. The method is further to useful for predicting efficacy of a drug in treating viral infection, plant genome shuffling, micropore manipulation, producing transgenic animals, improvement of overexpressed genes for a desired phenotype and the mathod are inseful in malant contractors. e method are useful in molecular genetics. This sequence represents coli reca protein clone used in the method of the invention. the method 898888888888888888888888888888888

of

Sequence 358 AA;

180 240 300 61 IVELYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSQPD 120 NLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLDIRRIGAVKEGENVVGS 246 99 TGEQALEICDALARSGAVDVIVVDSVAALTPKAEIEGEIGDSHMGLAARMMSQAMRKLAG ETRVKVVKNIKIAAPFKQAEFQILYGEGINFYGELVDLGVKEKLIEKAGAWYSYKGEKIGQ 1 AIDENKOKALAAALGQIEKOFGKGSIMRLGEDRSMDVETISTGSLSLDIALGAGGLPMGR NLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLDIRRIGAVKEGENVVGS 7 AIDENKQKALAAALGQIEKQPGKGSIMRLGEDRSMDVETISTGSLSLDIALGAGGLPMGR ö 100.0%; Score 1678; DB 8; Length 358; 100.0%; Pred. No. 6.3e-155; ive 0; Mismatches 0; Indels 0 GKANATAWLKDNPETAKEIEKKVRELLLSNPNSTP 341 GKANATAWLKDNPETAKEIEKKVRELLLSNPNSTP 335 Query Match Best Local Similarity 100. Matches 335; Conservative 121 187 247 307 181 241 301 셤 g 임 g g ઠે ઠે ò Š ò

RESULT 8

ADQ87821 standard; protein; 358 AA

ADQ87821;

09-SEP-2004 (first entry)

E. coli recA protein.

RecA; protoplast formation; gamete; heat tolerance; ethanol production; ethanol tolerance; enzyme cofactor; NAD(P)H; glucose transport; meiosis; heterokaryon; taxol; cyclosporin A; erythromycin; viral infection; plant genome shuffling; micropore manipulation; reiterative pooling.

121 TGEQALEICDALARSGAVDVIVVDSVAALTPKAEIEGEIGDSHMGLAARMASQAMRKLAG 180

99

7 AIDENKQKALAAALGQIEKQFGKGSIMRLGEDRSMDVETISTGSLSLDIALGAGGLPMGR 61 IVEIYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSQPD

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1 AIDENKQKALAAALGQIEKQFGKGSIMRLGEDRSMDVETISTGSLSLDIALGAGGLPMGR

Matches 335; Conservative

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Indela

Escherichia

AU2004200501-A1.

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The invention relates to a method of evolving cells to acquire a desired property by forming protoplasts of different cells, fusing the protoplasts of protoplasts to come hybrid protoplasts from the protoplasts from the protoplasts in which coprotoplasts to form hybrid protoplasts in which capenemes from protoplasts to form additional hybrid genomes and incubating additional hybrid protoplasts form additional hybrid genomes and incubating additional hybrid protoplasts for genomes from protoplasts recombine to form additional hybrid genomes and incubating additional hybrid protoplasts form additional hybrid genomes and incubating additional hybrid protoplasts form additional hybrid genomes and incubating additional hybrid protoplasts form additional hybrid genomes and incubating deference and the feather strains of a species or different genetes for producing a pool of the female genetes, permitting at least a portion of the certilised genetes, permitting at least a portion of the resulting fertilised genetes, permitting at least a portion of the centilised genetes, permitting at least a portion of the centilised genetes, permitting and selecting the library for a cquired train or property. The methods are useful for evolving cells to cquired easired properties such as heat tolerance, ethanol production, cthanol tolerance, improved production and maintenance of enzyme cofactors, improved production and maintenance of NAD(P)H and improved production and maintenance of NAD(P)H and improved cofactors, improved production and maintenance of NAD(P)H and improved care secondary metabolite, the secretion of a procein or transpired erransport. The desired properties such as enhanced recombination, careful for explaints and erythromychin. The method is also useful for predicting efficacy of a drug in treating viral pernome shuffling, micropore mainpulation, producing transgenic contarned pernome shuffling, micropore maintenance organisms. The method are useful in molecular genetics. This sequence contary metabolity and t
                                                                                                                                                                                                                                                                                                                  Evolving cells to acquire a desired property, by forming protoplasts different cells, fusing protoplasts to form hybrid protoplasts (HP), producing regenerated cells, forming additional HP and producing additional regenerated cells.
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Subramanian V;
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100.0%; Pred. No. 6.3e-155;
iive 0; Mismatches 0;
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Krebber
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Zhang Y, Krebbe
Del Cardayre S;
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                                     09-FEB-2004; 2004AU-00200501.
                                                                                  09-FEB-2004; 2004AU-00200501
                                                                                                                                                                     Bass S,
lisman G,
                                                                                                                                                                                           Affholter JA, Huisman G,
Minshull J, Stemmer WPC,
                                                                                                                                                          Cox T, Base T
                                                                                                                             (MAXY-) MAXYGEN INC.
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N-PSDB; ADQ87814.
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04-MAR-2004
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12-AUG-2004
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                                                                                      Query Match
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(EGGL/)
(HARU/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a hyperrecombinogenic recA protein. The wild type recA protein (APK50827) was used to produce hyperrecombinogenic variants, using the method of the invention. The specification describes a method for producing a library of diverse multicellular organisms using pools of male and female gametes. At least one of the male pool or female pools of male and female gametes. At least one of the male pool or female pools of different gametes derived from different strains of a species or of different species. The viable organisms is produced from the fertilized gametes are repeatedly crossed to produce a library of diverse organisms, which are selected for a desired trait or property. The methods can be used to evolve calls to acquire a desired composerty such as heat tolerance, ethanol production or tolerance, acid, improved production and maintenance of enzyme cofactors or NAD(P)H and improved broduction and maintenance of enzyme expression of a protein or primary or secondary metabolite. Alternatively the desired
                                                                                      recA; hyperrecombinogenic variant; male gamete; female gamete;
heat tolerance; ethanol production; ethanol tolerance; metabolite; taxol;
cyclosporin A; erythromycin; meiosis.
127 TGEQALEICDALARSGAVDVIVVDSVAALTPKAEIEGEIGDSHMGLAARMMSQAMRKLAG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stemmer WPC, Ness JB, Minshull J;
Castle LA, Krebber CM, Bass S, Zhang Y;
Affholter JA;
                                    ETRVKVVKNKIAAPFKQAEFQILYGEGINFYGELVDLGVKEKLIEKAGAWYSYKGEKIGQ
                        NLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLDIRRIGAVKBGENVVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Evolution of whole cells and organism by iterative cycles of recombination and selection and screening for acquisition of desired properties.
                                                                                                                                                                                                                                                                                Amino acid sequence of a hyperrecombinogenic recA protein clone 6.
                                                                                                                       GKANATAWLKDNPETAKEIEKKVRELLLSNPNSTP 335
                                                                                                                                       GKANATAWLKDNPETAKEIEKKVRELLLSNPNSTP 341
                                                                                                                                                                                                                                                                                                                                                                                                                     note= "encoded by TCG"
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                                                                                                                                                                                                         AAY68831 standard, protein, 358 AA
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Patten PA, Subramanian V,
Cox T, Huisman G, Yuan L,
                                                                                                                                                                                                                                                         (first entry)
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N-PSDB; AAZ60613.
                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli.
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Misc-difference
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property is secretion of a protein or secondary metabolite, chosen from taxol, cyclosporin A and erythromycin. The desired property may be a capacity for meiosis or compatibility to form a heterokaryon with another
                                                                                                                                                                                                                                                                                                                                                                                                              126
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                                                                                                                                                                                                                       Gaps
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DNA strand exchange reaction; site-specific cleavage; mutant; mutein.
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                                                                                                                                                                  Length 358;
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                                                                                                                                                                  99.9%; Score 1677; DB 3;
99.7%; Pred. No. 7.9e-155;
iive 1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key Location/Qualifiers Misc-difference 38
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                                                                                                                                                                                         Best Local Similarity 99.7
Matches 334; Conservative
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LUSETTI S L.
EGGLER A L.
HARUTA N.
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N-PSDB; ADR16431.
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                                                                                                                     Sequence 358 AA;
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recursive sequence recombination; evolution

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protein is either a single mutant Rech protein comprising a deletion of amino acid residues from the carboxyl terminus, or a double mutant Rech protein comprising a deletion of amino acid residues from the carboxyl terminus, or a double mutant Rech protein comprising a deletion of amino acid residues from the carboxyl terminus and an amino acid change from a gultamate to a basic amino acid. The invention also relates to a polymucleotide sequence that encodes the Rech mutant protein, a method of catalysing an in vitro homologous DNA pairing and DNA strand exchange reactions in of the Rech mutant protein and a method of increasing recombination of the Rech mutant protein and a method of increasing recombination of efficiency of homologous DNA pairing and DNA strand exchange reactions in comprising supplying to the cell an amount of the Rech mutant protein as compared to wild-type Rech. The DNA binding protein is the sapNA binding protein from Escherichia coli (SSB). It also comprises enhanced binding protein from Escherichia coli (SSB). It also comprises enhanced binding protein from Escherichia coli (SSB). Creaction as compared to wild-type Rech. The DNA creaction as compared to wild-type Rech. The composition and methods are reactions in an in vitro or in vivo environment. These may be used in promoting in vitro alterations of genes to permit the rapid construction of the mutant proteins may also be used in targeting the site-specific cleavage of mutant proteins passed in targeting the site-specific cleavage continy enterminate proteins as a basis for the design and construction of circuits based on DNA. This sequence represents a Rech
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New RecA mutant proteins comprising a single mutation or a double mutation, useful for catalyzing homologous DNA pairing and DNA strand exchange reactions in an in vitro or in vivo environment.
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                                                                                                                                        relates to an isolated RecA mutant protein, where the
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99.7%; Pred. No. 1.4e-154;
iive 1; Mismatches 0;
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                                                                                            Claim 13; SEQ ID NO 3; 34pp; English
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Matches 334; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 335 AA;
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Escherichia coli; recA protein; hyperrecombinogenic variant; Minshall;

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The present invention provides methods employing iterative cycles of recombination and selection/screening for evolution of whole cells and organisms toward acquisition of desired properties, e.g. enhanced recombinosenicity, genome copy number, and capacity for expression and/or secretion of proteins and secondary metabolites. The present sequence represents a wild-type recA protein (designated new Minshall), from an example of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Evolution of whole cells and organisms by recursive DNA sequence recombination in cells to evolve cells having acquired desired function, useful in methods for predicting the efficacy of a drug in treating viral or pathogenic infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 AIDENKQKALAAALGQIEKQFGKGSIMRLGEDRSMDVETISTGSLSLDIALGAGGLPMGR
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                                                                                                                                                                                           Minshull J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 358;
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                                                                                                                                                                                            Ness JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1674; DB 2;
Pred. No. 1.6e-154;
1; Mismatches 0;
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                                                                                                                                                                                            Tobin MB, Stemmer WPC,
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                                                                                                                                                                                                                                                                                                                                                    Example 1; Fig 13; 125pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.8%;
                                                                                                           98WO-US000852.
                                                                                                                                      97US-0035054P.
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Best Local Similarity 99.7
Matches 334; Conservative
                                                                                                                                                                                                                                       WPI; 1998-427565/60.
                                                                                                                                                                  (MAXY-) MAXYGEN INC.
                         Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 358 AA;
                                                                                                                                                                                                                                                       N-PSDB; AAV44285
                                                                                                                                                                                               Delcardayre SB,
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                                                                                                                                       17-JAN-1997;
                                                                                                           16-JAN-1998;
                                                     WO9831837-A1
                                                                               23-JUL-1998.
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ID AAY6
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The present sequence represents a hyperrecombinogenic recA protein. The wild type recA protein. (AAY68827) was used to produce hyperrecombinogenic variants, using the method of the invention. The specification describes a method for producing a library of diverse multicallular organisms using pools of male and female gametes. At least one of the male pool or female pools of male and female gametes. At least one of the male pool or female pools comprises a number of a different species. The wiable organisms to pools comprises or of a different species. The viable organisms of a species or of a different species. The viable organisms of produce from the fertilized gametes are repeatedly crossed to produce a library of diverse organisms, which are selected for a desired trait or property. The methods can be used to evolve cells to adust a desired improved production and maintenance of enzyme cofactors or NAD(P)H and improved glucose transport. The desired property may be expression of a protein or primary or secondary metabolite. Alternatively the desired property is secretion of a protein or secondary metabolite, chosen from taxol, cyclosporin A and erythromycin. The desired property may be a capacity for meiosis or compatibility to form a heterokaryon with another
                                                         rech, hyperrecombinogenic variant; male gamete; female gamete;
heat tolerance; ethanol production; ethanol tolerance; metabolite; taxol;
cyclosporin A; erythromycin; meiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                           Stemmer WPC, Ness JE, Minshull J;
Castle LA, Krebber CM, Bass S, Zhang Y;
Affholter JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Evolution of whole cells and organism by iterative cycles of recombination and selection and screening for acquisition of desired
                   Amino acid sequence of a hyperrecombinogenic recA protein clone 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Fig 13; 197pp; English.
                                                                                                                                                                                                                                                                                                99WO-US015972.
                                                                                                                                                                                                                                                                                                                                          98US-00116188.
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Cox T, Huisman G, Yuan L,
                                                                                                                                                                                                                                                                                                                                                                                                                             Del Cardayre S, Tobin M,
                                                                                                                                                                                                                                                                                                                                                                                   (MAXY-) MAXYGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-182446/16
                                                                                                                                                                       Escherichia coli.
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                                                                                                                                                                                                              WO200004190-A1
                                                                                                                                                                                                                                                                                              15-JUL-1999;
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                                                                                                                                                                                                                                                      27-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          properties.
                                                                                                                                                 Synthetic
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1 AIDENKOKALAAALGQIEKOFGKGSIMRLGEDRSMDVETISTGSLSLDIALGAGGLPMGR Gaps ; Length 358; 1; Indels 99.7%; Score 1673; DB 3; 99.4%; Pred. No. 1.9e-154; iive 1; Mismatches 1; Best Local Similarity 99.4 Matches 333; Conservative Query Match g ઠે

121

ઠે 셤 ò 셤 ઠે

181

Sequence 358 AA;

ETRVKVVKNKIAAPFKQAEFQILYGEGINFYGELVDLGVKEKLIEKAGAWYSYKGEKIGQ 300 335 307 GKANATAWLKDNPETAKEIEKKVRELLLSNPNSTP 301 GKANATAWLKDNPETAKEIEKKVRELLLSNPNSTP 241 RESULT 13 ADQ87823 g ð 셤 ò

RecA; protoplast formation; gamete; heat tolerance; ethanol production; ethanol tolerance; enzyme cofactor; NAD(P)H; glucose transport; meiosis; heterokaryon; taxol; cyclosporman, a; erythromycin; viral infection; plant genome shuffling; micropore manipulation; reiterative pooling. E. coli recA protein clone #2. (first entry) 09-SEP-2004

ADQ87823 standard; protein; 358 AA.

ADQ87823;

Escherichia coli.

AU2004200501-A1.

04-MAR-2004.

09-FEB-2004; 2004AU-00200501.

09-FEB-2004; 2004AU-00200501.

(MAXY-) MAXYGEN INC.

Tobin M; Ness JE, Tobin Subramanian V; Castle LA, Patten PA, Zhang Y, Krebber CM, Del Cardayre S; Yuan L, Cox T, Bass S, Affholter JA, Huisman G, Minshull J, Stemmer WPC,

2004-507924/49. WPI; 2004-507924/ N-PSDB; ADQ87816. Evolving cells to acquire a desired property, by forming protoplasts of different cells, fusing protoplasts to form hybrid protoplasts (HP), producing regenerated cells, forming additional HP and producing additional regenerated cells.

Disclosure, Fig 13; 196pp; English.

The invention relates to a method of eviving cells to additing the property by forming protoplasts of different cells, fusing the protoplasts to form hybrid protoplasts, incubating the hybrid protoplasts from regenerated cells, fusing protoplasts to form hybrid protoplasts from regenerated cells, fusing protoplasts to form hybrid protoplasts in which genomes from protoplasts recombine to form hybrid protoplasts in which cell conclusions additional hybrid genomes and cells. The invention also relates to a method of producing a library of diverse multicellular organisms involving providing a pool of cells invention also relates to a method of producing a library of diverse multicellular organisms involving providing a pool of the female gametes and a pool of fiderent strains of a species or different species and the male gametes of certilise the female gametes, bermitting at least a portion of the centuring fertilise dametes to grow into reproductively viable organisms to organisms, repeatedly crossing the reproductively viable organisms to organisms, repeatedly crossing the reproductively viable organisms to desired properties such as heat tolerance, ethanol production, ethanol tolerance, improved production and maintenance of enzyme cofactors, improved production and maintenance of enzyme cofactors, improved production and maintenance of may a protein or primary metabolite or secondary metabolite, the secretion of a protein or invention relates to a method of evolving cells to acquire a desired

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secondary metabolite, capacity for meiosis or compatibility to form a heterokaryon with another strain. The secondary metabolite is chosen from taxol, cyclosporin A and erythromycin. The method is also useful for acquisition of desired properties such as enhanced recombinogenicity, gene copy number or gene reductivity and capacity for expression and/or secretion of proteins or secondary metabolites. The method is further useful for predicting of escondary metabolites. The method is further useful for predicting micropore manipulation, producing transgenic animals, improvement of overexpressed genes for a desired phenotype and reiterative pooling and breeding of higher organisms. The cells evolved by the method are useful in molecular genetics. This sequence represents an E. coli recA protein clone used in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 TGEGALBICDALARSGAVDVIVVDSVAALTPKAEIEGEIGDSHMGLAARMMSQAMRKLAG 186
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                                                                                                                                                                                                                                                                                                                                                                          7 AIDENKQKALATALGQIEKQFGKGSIMRLGEDRSMDVETISTGSLSLDIALGAGGLPMGR
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                                                                                                                                                                                                                                                                                                                                                                                                                         61 IVELYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSQPD
                                                                                                                                                                                                                                                                                                                Gaps
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Subramanian V;
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0
                                                                                                                                                                                                                                                                              Length 358;
                                                                                                                                                                                                                                                                                                                Indels
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Krebber CM,
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                                                                                                                                                                                                                                                                              Score 1673; DB 8;
Pred. No. 1.9e-154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKANATAWLKDNPETAKEIEKKVRELLLSNPNSTP 335
                                                                                                                                                                                                                                                                                                                  1; Mismatches
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Zhang Y,
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                                                                                                                                                                                                                                                                                99.7%;
99.4%;
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Huisman G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                     Best Local Similarity 99.4
Matches 333; Conservative
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                                                                                                                                                                                                                                                                                                   Local Similarity
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Affholter JA, F
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                                                                                                                                                                                                                                             Sequence 358 AA;
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corporate by forming protoplasts of different cells, fusing the protoplasts to form hybrid protoplasts, incubating the hybrid protoplasts to protoplasts to form hybrid protoplasts, incubating the hybrid protoplasts to protoplasts from protoplasts to form hybrid protoplasts to form hybrid protoplasts in which regenerated cells, fusing protoplasts to form hybrid protoplasts in which regenerated cells, fusing protoplasts for producing additional hybrid protoplasts for producing additional protoplasts for producing additional protoplasts for producing additional hybrid protoplasts for producing additional protoplasts for producing additional hybrid protoplasts for producing additional hybrid protoplasts for producing additional hybrid protoplasts for producing additional hybrid protoplasts for producing additional hybrid protoplasts for enganes and page feed a molicial protoplasts for a method of producing a pool of female gametes where one of the male pool or male gametes bad spaces or different species and the male gametes for the female pool comprises several different species and the male gametes for the female pool comprises several different species and the male gametes for esculping fertilised gametes, permitting at least a portion of the certain property. The methods are useful for evolving cells to general properties such as heat tolerance, ethanol production, and maintenance of enzyme cells of properties such as heat tolerance, ethanol production, improved production and maintenance of enzyme cells of properties such as heat tolerance, ethanol production, and maintenance of caryme conference, improved production and maintenance of enzyme that protein and maintenance of enzyme that protein and expensive production and maintenance of caryme conference, improved production and maintenance of enzyme that secondary metabolite, capacity for metabolite, the secretion of a protein of desired proteins or secondary metabolite, capacity for metabolite, the method is also useful for predicting of from engage and a se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLDIRRIGAVKEGENVVGS 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               by the method are useful in molecular genetics. This sequence represents an B. coli recA protein clone used in the method of the invention.
                                                                                                                                                                                                                                                                    invention relates to a method of evolving cells to acquire a desired
                                                                                                         Bvolving cells to acquire a desired property, by forming protoplasts of different cells, fusing protoplasts to form hybrid protoplasts (HF), producing regenerated cells, forming additional HP and producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AIDENKOKALAAALGQIEKQFGKGSIMRLGEDRSMDVETISTGSLSLDIALGAGGLPMGR
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Pred. No. 4.8e-154;
1; Mismatches 1;
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Del Cardayre
                                                                                                                                                                                                                              Disclosure; Fig 13; 196pp; English.
                                                                                                                                                             producing regenerated cells, additional regenerated cells.
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Best Local Similarity 99.4%;
Matches 333; Conservative
    Stemmer WPC,
                                                 2004-507924/49.
                                                                      N-PSDB; ADQ87819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 358 AA;
    Minshull J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Evolution of whole cells and organisms by recursive DNA sequence recombination in cells to evolve cells having acquired desired function, useful in methods for predicting the efficacy of a drug in treating viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180
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                                                                                                                                                                                                                    Escherichia coli; recA protein; hyperrecombinogenic variant; Minshall; recursive sequence recombination; evolution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 NLKQSNTLLIFINQIRWKIGVMFGNPETTTGGNALKFYASVRLDIRRIGAVKEGENVVGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 99.4%; Score 1668; DB 2; Length 3: Best Local Similarity 99.1%; Pred. No. 6e-154; Matches 332; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ness JE,
                                                                                                                                                                                          Hyperrecombinogenic variant recA protein clone 4.
 GKANATAWLKDNPETAKEIEKKVRELLLSNPNSTP 335
                  307 GKANATAWLKDNPETAKEIEKKVRELLLSNPNSTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stemmer WPC,
                                                                                                   AAW64215 standard; protein; 358 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                 97US-0035054P
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                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or pathogenic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                              (MAXY-) MAXYGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-427565/60.
N-PSDB; AAV44287.
                                                                                                                                                                                                                                                                  Escherichia coli.
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                                                                                                                                                             28-APR-1999
                                                                                                                                                                                                                                                                                                             WO9831837-A1
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                                                                                                                                                                                                                                                                                  Synthetic.
301
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        Qy
        241 ETRVKVVKOKIAAPFKQAEFQILYGEGINFYGELVDLGVKEKLIEKAGAWYSYKGEKIGQ 300

        Db
        247 ETRVKVVKOKIAAPPFKQAEFQILYGEGINFYGELVDLGVKEKLIEKAGAWYSYKGEKVGQ 300

        CQy
        301 GKANATAWLKDNPETAKEIEKKVRELLLSNPNSTP 335

        Db
        307 GKANATAWLKDNPETAKEIEKKVRELLLSNPNSTP 341
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Search completed: February 16, 2006, 01:18:51 Job time : 135 secs

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5.1.7
Biocceleration Ltd.
 GenCore version (c) 1993 - 2006
            Copyright
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OM protein - protein search, using sw model

Febrúary 16, 2006, 01:19:09; Search time 25.5 Seconds (without alignments) 1264.024 Million cell updates/sec Run on:

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1 AIDENKQKALAAALGQIEKQ........AKEIEKKVRELLLSNPNSTP 335 US-10-733-782-1 Perfect score: Sequence:

1 3. **BLOSUM62** Scoring table:

283416 segs, 96216763 residues Searched:

Gapop 10.0 , Gapext 0.5

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:*
1: pir1:*
1: pir2:*
1: pir3:*
: pir4:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

BS	rip	recombination prot	_			protein	c	recombination prot	recombination prot	recA protein VC054	recombination prot	recombination prot	recombination prot	recombination prot		recombination prot	recombination prot	recombination prot	recA protein - Pse	recombination prot	recombination prot	recombination prot	recombination prot	recA protein NMB14	RecA protein NMA16	recA protein [impo	Dination	recombination prot	recombination prot	recombination prot
SUMMARIES			3	7	9	7	7	9	Σ	0	4	-	6	89	Æ	7	9	0	0	9	6	6	8	7	0	0	S	9	υ	7
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	Query Match	0	100.0	99.3	97.8	91.4	91.3	91.2	9.68			84.2	79.4	78.8	75.6	75.4	75.4	74.9	74.8	74.5	4		•	ä	72.5			•	71.6	71.5
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AH2806	G97585	140347	ROBCAT	JN0639	S16898	B82844	JC4718	S17782	S10499	841560	S49464	C87384	T35139	S38674	A55528
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363	416	360	346	348	348	347	343	360	352	343	355	356	374	374	340
71.5	71.5	71.4	70.8	9.07	70.5	70.1	70.0	69.1	68.89	68.7	9.89	68.2	68.1	68.1	61.9
1200.5	1200.5	1198.5	1187.5	1184	1183.5	1177	1174	1160	1154	1153.5	1150.5	1145	1143	1143	1140
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Cispecies: Escherichia coli

Cispecies: Escherichia coli

Cispecies: Escherichia coli

Cispecies: Escherichia coli

Cispecies: Escherichia coli

Cispecies: Escherichia coli

Cispecies: Escherichia coli

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Cispecies: Escherichia coli

Cispecies: In-ful-1900 #sequence revision 14-Nov-1997 #text change 09-Jul-2004

Cispecies: In-ful-1900 #sequence revision 14-Nov-1997 #text change 09-Jul-2004

Cispecies: In-ful-1900 #sequence revision 14-Nov-1997 #text change 09-Jul-2004

Cispecies: In-ful-1900 #sequence III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;

A; Rose, D.J.; Mau, B.; Shao, Y.

A; Reference D.J.; Mau, B.; Shao, Y.

A; Reference number: A64720; MUD:97426617; PMID:9278503

A; Residues: In-33 * cBLAT>

A; Molecule type: DNA

A; Residues: 1-33 * cBLAT>

A; Residues: 1-33 * cBLAT>

A; Cross-references: UNIPROT: P03017; UNIPARC:UPI0000112C1C; GB:AE000354; GB:U00096; NID

A; Experimental source: strain K-12, substrain MG1655

B; Horii, T.; Ogawa, T.; Ogawa, T.;

Proc. Natl: Acad. Sci. U.S.A. 77, 313-317, 1980

A; Title: Organization of the recA gene of Escherichia coli.

A; Residues: 2-353 * cHOR;

A; Residues: 2-353 * cHOR;

A; Residues: 2-353 * cHOR;

A; Residues: 2-353 * cHOR;

A; Residues: 2-353 * cHOR;

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A; Residues: 2-353 * cHOR;

A; Residues: 2-353 * cHOR;

A; Residues: 2-350 * cHOR;

A; Residues: 2-350 * cHOR;

A; Residues: 2-350 * cHOR recombination protein recA [validated] - Escherichia coli (strain K-12)

A;Cross-references: UNIPARC:UPI0000112C17; GB:V00328; NID:g42672; PIDN:CAA23618.1; PID R;Sancar, A.; Stachelek, C.; Konigsberg, W.; Rupp, W.D. Proc. Natl. Acad. Sci. U.S.A. 77, 2611-2615, 1980
A;Title: Sequences of the recA gene and protein.
A;Reference number: A93846; MUID:80234673; PMID:6930655

A;Molecule type: DNA
A;Residues: 2-333 <cSAN>
A;Residues: 2-333 <cSAN>
A;Residues: 2-333 <cSAN>
A;Cross-references: UNIPARC:UPI0000112C17; GB:V00328; GB:J01672; NID:G942672; PIDN:CAA23
R;Zhao, X.J.; McEntee, K.
B;Zhao, X.J.; McEntee, K.
B;Zhao, X.J.; McEntee, K.
A;J. Center: 222, 369-376, 1990
A;Title: DNA sequence analysis of the recA genes from Proteus vulgaris, Erwinia carotov
A;Reference number: S11931; MUID:91109725; PMID:2274037

A; Accession: S11931 A; Molecule type: DNA

A; Residues: 2-353 <ZHA>
A; Residues: 2-553 <ZHA>
A; Cross-references: UNIPARC:UPI0000112C17; GB:X55552; NID:942678
A; Cross-references: Universe of the contracted in GenBank entry ECRECAGEN, release 109.0
R; Morimatsu, K.; Horii, T.
R; Morimatsu, K.; Horii, T.
Biochem: 234, 695-705, 1995
A; Title: DNA-binding surface of RecA protein. Photochemical cross-linking of the first A; Reference number: 863525; MUID:96096752; PMID:8529655

A;Accession: S63525 A;Status: preliminary A;Molecule type: protein A;Residues: 65-69;90-97;179-184;200-207;258-265;304-311;323-331 <MOR1> A;Cross-references: UNIPARC:UPI00001748A7; UNIPARC:UPI00001748A8; UNIPARC:UPI00001748A9

Gaps

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9 61 121

120

181

240 241

180

300

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DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: D91073
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Rossides: 1-553 < HAX>
A;Cross-references: UNIPROT: P03017; UNIPARC: UPI0000112C1C; GB:BA000007; PIDN:BAB36979.1, A;Experimental source: strain O157:H7, substrain RIMD 0509952
A;Genetics:
A;Genetics:
C;Superfamily: recombination protein recA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: H85917
R;Perra, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2011
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: H85917
A;Accession: H85917
A;Molecule type: DNA
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A,Experimental source: strain O157:H7, substrain ED1933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 ETRVKVVKNKIAAPPKQAEFQILYGEGINFYGELVDLGVKEKLIEKAGAWYSYKGEKIGG 301
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 353;
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99.3%; Score 1666; DB 2; Length 3:
Best Local Similarity 99.4%; Pred. No. 3e-105;
Matches 333; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 1678; DB 2; Best Local Similarity 100.0%; Pred. No. 4.6e-106; Matches 335; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 GKANATAWLKDNPETAKEIEKKVRELLLSNPNSTP 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Gene: recA
C, Superfamily: recombination protein recA
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R; Morimatsu, K.; Horii, T.

Bur. J. Blochem. 228, 772-778, 1995

A; Title: The DNA-binding site of the RecA protein. Photochemical cross-linking of Tyrlo3

A; Reference number: 869129; MUD:9525284; PMID:7737176

A; Reference number: 869129

A; Scatus preliminary

A; Molecule type: protein

A; Residues: 90-108, 180-184

A; Cross-references: UNIPARC:UPIO0001748AE

R; Gardner, R. V.; Voloshin, O. N.; Camerini-Otero, R.D.

Bur. J. Biochem. 233, 419-425, 1995

A; Accession: 863799

A; Molecule type: protein

A; Residues: 377-199, 192-194 <GAR>
A; Accession: 863799

A; Molecule type: protein

A; Residues: 377-199, 192-194 <GAR>
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A; Molecule type: protein

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A; Molecule type: protein

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A; Molecule type: protein

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A; Molecule type: protein

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A; Molecule type: protein

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A; Molecule type: protein

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A; Molecule type: protein

A; Residues: 377-199, 192-184

A; Molecule type: protein

A; Residues: 377-199

A; Molecule type: protein

A; Residues: 377-199

A; Molecule type: protein

A; Residues: 4-157; 166-195; 211

A; A; Residues: 40-148

A; Residues: 40-157; 166-195; 211

A; A; Residues: 40-157; 198-184

A; Molecule type: protein

A; Residues: 58 min

C; Mulpa; Dana, 193

A; Description: 58 min

C; Mulpa; Dana, 194

A; Description: 1919, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910, 1910
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D91073
C.GA protein [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
C.Species: Bscherichia coli
C.Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C.Accession: D91073
E.Hayasahi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
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; Pred. No. 4.6e-106;
0; Mismatches 0;
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C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Date: 02-Nov-2001 #N: Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Reference number: DNA
A;Residues: 1-356 <KUR>
A;Residues: 1-356 <KUR>
A;Residues: 1-356 <KUR>
A;Cross-references: UNIPROT:P37858; UNIPARC:UP10000165AF8; GB:AL590842; PIDN:CAC92539.1
C;Genetics:
A;Gene: recA
C;Superfamily: recombination protein recA
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                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
91.4%; Score 1534; DB 2; Length 3
Best Local Similarity 91.9%; Pred. No. 2.4e-96;
Matches 305; Conservative 14; Mismatches 13; Indels
  protein [imported] - Yersinia pestis (strain C092)
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A;Residues: 1-353 cPAR>
A;Residues: 1-353 cPAR>
A;Crossion: AP08535.1; PID:g16503906;
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                                                                                                                                 NLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLDIRRIGAVKEGENVVGS
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ilarity 97.3%; Pred. No. 1.4e-103;
Conservative 5; Mismatches 4;
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C,Superfamily: recombination protein recA
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Best Local Simil
Matches 326; C
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Gaps

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Length 356;

9 61 121

180

240 241 301

recombination protein recA - Enterobacter agglomerans
Nalternate names: recombinase
Nalternate names: recombinase
C;Species: Enterobacter agglomerans
C;Species: Enterobacter agglomerans
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S11481
R;Rappold, C.S.J.; Klingmueller, W.
submitted to the EMBL Data Library, January 1993
A;Description: Cloning and sequencing of the recA gene from Enterobacter agglomerans 33
A;Reference number: S31481
A;Status: preliminary
A;Accession: S31481
A;Status: preliminary
A;Residues: 1-354 <RAP>
A;Coss-references: UNIPROT: P33037; UNIPARC: UPI000016EC3A; GB:L03291; EMBL: Z19517; NID:
C;Genetics: A,Gene: recA S,Superfamily: recombination protein recA C;Superfamily: recombination; DNA recombination; DNA repair; nucleotide binding; P-loop C;Keywords: ATP; DNA binding; DNA recombination; DNA repair; nucleotide binding; P-loop F;67-74/Region: nucleotide-binding motif B F;141-146/Region: nucleotide-binding motif B F;73/Binding site: ATP (Lys) #status predicted 91.3%; Score 1532; DB 2; Length 354; Query Match

RESULT AG0401

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A; Molecule type: DNA
A; Residues: 1-355 cAKA>
A; Residues: 1-355 cAKA>
A; Residues: 1-355 cAKA>
A; Residues: 1-355 cAKA>
A; Residues: 1-355 cAKA>
A; Residues: 1-355 cAKA>
A; Conserved conserved
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Conserved conserved
C; Superfamily: recombination protein recA
C; Superfamily: recombination protein recA
C; Superfamily: recombination protein recA
C; Superfamily: recombination moteling recombination; DNA repair; nucleotide binding; P-loop;
F; G7-74/Region: nucleotide-binding motif A (P-loop)
F; H4/Region: nucleotide-binding motif B
F; H3/Binding site: ATP (Lys) #status predicted
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C;Species: Vibrio cholerae
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: E82310
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.
C;Accession: D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Wekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
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                                                                                                                                                                                           recombination protein recA - Proteus mirabilis
NyAlternate names: recombinase A
C;Species: Proteus mirabilis
C;Species: Proteus mirabilis
C;Accession: S04606
R;Akaboshi, E.; Yip, M.L.R.; Howard-Flanders, P.
Nucleic Acids Res. 17, 4390, 1989
A;Title: Nucleotide sequence of the recA gene of Proteus mirabilis.
A;Reference number: S04606; MUID:89296502; PMID:2544862
A;Accession: S04606.
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Matches 295; Conservative
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recombination protein recA - Yersinia pestis
NiAlternate names: recombinase A
C;Species: Versinia pestis
C;Species: Versinia pestis
C;Species: Versinia pestis
C;Species: Versinia pestis
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S37586
R;Kryukov, V.M.; Suchkov, I.Y.; Sazykin, I.S.; Mishankin, B.N.
submitted to the EMBL Data Library, October 1993
A;Description: Complete nucleotide sequence of Yersinia pestis recA gene.
A;Reference number: S37586
A;Accession: S37586
A;Accession: S37586
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-356 < KRY>
A;Cross-references: UNIPROT:P37858; UNIPARC:UP10000170617; EMBL:X75336; NID:g406793; PIC
C;Genetics:
C;Genetics:
A;Gene: recA
C;Superfamily: recombination protein recA
C;Superfamily: recombination protein recA
C;Superfamily: nucleotide-binding motif A (P-loop)
F;67-74/Region: nucleotide-binding motif B
F;73/Binding site: ATP (Lys) #status predicted
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                            Indels
        92.1%; Pred. No. 3.3e-96; ive 15; Mismatches 11;
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91.2%; Score 1530; DB 2;
Best Local Similarity 91.9%; Pred. No. 4.6e-96;
Matches 305; Conservative 14; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GKANATAWLKDNPETAKEIEKKVRELLLS 329
                              303; Conservative
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Appreciaes: Vibrio anguillance Actions of the reck gene of Vibrio anguillance makes: Teconage of Accession: Odd 461

R, Accession: Odd 461

R, Accession: Odd 461

R, Tolmasky, M.E.; Gammie, A.E.; Crosa, J.H.
Gene 110, 41-48, 1992

A, Title: Characterization of the reck gene of Vibrio anguillarum.
A, Tatle: Characterization of the reck gene of Vibrio anguillarum.
A, Recession: Odd 461

A, Molecule type: DNA
A, Residues: 1-348 < TOL>
A, Rocession: Odd 461

A, Molecule type: DNA
A, Residues: 1-348 < TOL>
A, Ferences: UNIPROT: P26348; UNIPARC: UPI0000133544; GB: M80525; NID: G155256; PIDP
A, Experimental source: strains 775 and 531A
A, Experimental source: strains 775 and 531A
C, Function:
A, Gene: reck
C, Function:
A, Gene: reck
C, Function:
A, Gene: reck
C, Function:
A, Gene: reck
C, Superfamily: recombination protein reck
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C, Superfamily: recombination protein reck
C, Superfamily: recombination mucleotide-binding motif A
F; 55-72 (Region: nucleotide-binding motif B
F; 256-279/Region: ATP binding #status predicted
F; 71/Binding site: ATP (Lys) #status predicted
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NiAlternate names: recombinase A
C:Species: Vibrio anguillarum
C:Spate: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
                                                                                                                                                                                   LKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLDIRRIGAVKEGENVVGSE
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                                                                                                                    121 GEQALEICDALARSGAVDVIVVDSVAALTPKAEIEGEMGDSHMGLQARMLSQAMRKLTGN
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84.2%; Score 1412.5; DB 2;
Best Local Similarity 83.6%; Pred. No. 3.8e-88;
Matches 276; Conservative 30; Mismatches 23;
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|KANACKYLKENPEIAKTLDKKLREMLLNPEN 331
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                                     A:Status: preliminary
A:Molecule type: DNA
A:Molecule type: DNA
A:Molecule type: DNA
A:Molecule type: DNA
A:Molecule type: DNA
A:Molecule type: DNA
A:Cross-references: UNIPARC:UPI000164B55; GB:AE004140; GB:AE003852; NID:g9654965; PIDN:A;Experimental source: serogroup Ol; strain N16961; biotype El Tor
C;Genetics:
C;Genetics:
A;Map position: 1
C;Superfamily: recombination protein recA
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C;Keywords: ATP: DNA binding; DNA recombination; DNA repair; nucleotide binding; P-loop;
F;65-2Kegion: nucleotide-binding motif A (P-loop)
F;139-144/Region: nucleotide-binding motif B
F;71/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             recombination protein recA - Vibrio cholerae
N.Alternate names: recombinase A
C.Species: Vibrio cholerae
C.Species: Vibrio cholerae
C.Stecies: 27-3na-1995 #sequence_revision 27-Jan-1995 #text_change 02-Feb-2001
C.Accession: S46274
R.Stroeher, U.H.; Lech, A.J.; Manning, P.A.
Mol. Gen. Genet. 244, 295-302, 1994
A.Title: Gene sequence of recA(+) and construction of recA mutants of Vibrio cholerae.
A.Reference number: S46274; MUID:94335880; PMID:8058040
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A;Molecule type: DNA
A;Residues: 1-354 «STR»
A;Cross-references: UNIPARC:UPI0000170586; EMBL:X71969; NID:9530269; PIDN:CAA50764.1;
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                                                                                                                                                                                                                                                                                                                  21; Indels
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A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: B82310
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83.1%; Pred. No. 1.9e-88;
ive 31; Mismatches 25;
                                                                                                                                                                                                                                                                   ; Score 1436; DB 2;
; Pred. No. 1.2e-89;
31; Mismatches 21;
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KANAYKYLKENPEIAKTLDKKLREMLLNPEN 389
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Best Local Similarity 84.3%;
Matches 279; Conservative 33
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Best Local Simi
Matches 275;
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- Aeromonas salmonicida
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Alternate names: recombinase A
C;Species: Aeromonas salmonicida
C;Date: 27-Feb-1997 #sequence_revision
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C;Function:
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                                                                                         RESULT 12
A49293
recombination protein recA - Haemophilus influenzae (atrain Rd KW20)
NiAlternate names: rec-I protein; recombinase A
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Date: 11-80-729; A64080
R;Species: Haemophilus influenzae
A;Reference number: A4929; MID:94042901; PMID:8226674
A;Reference number: A4929; MID:94042901; PMID:8226674
A;Residues: 1-54 42UL
A;Reserence: UNIRROT:P43705; UNIPRC:UD10001314E8; GB:L07529; NID:g305381; PIDN:A;Reses-reference: UNIRROT:P43705; UNIPRC:UD10001314E8; GB:L07529; NID:g305381; PIDN:A;Reses-reference: UNIRROT:P43705; UNIPRC:UD10001314E8; GB:L07529; NID:g305381; PIDN:A;Residues: 1-54 42UL
A;Residues: L.54 42UL
A;Residues: L.54 42UL
A;Residues: L.55 42UL
A;Residues: L.55 42UL
A;Reference number: R.D: Fritchman, J.L.; Glodek, A.; Kallay, J.M.; Weidman, J.D.; Science 269, 466-512, 1995
A;Attle: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Retues: nucleic acid sequence not shown; translation not shown
A;Reference number: A64000; WUD:95350630; PMID:754280
A;Attle: whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Residues: L-54 4TKR
A;Residues: L-54 4TKR
A;Residues: L-54 4TKR
A;Residues: L-54 4TKR
A;Residues: L-54 4TKR
A;Residues: L-54 4TKR
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||||| :|:|| | :: |:|| || KANACKFLRENPAAMALDTKLREMLL-NP
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Cyaccesion: UC5198
R;Umelo, B.; Noonan, B.; Truet, T.J.
Reference number: JC5198, MUID:97074662; PMID:8917089
A;Reference number: JC5198, MUID:97074662; PMID:8917089
A;Accession: UC5198
A;Accession: UC5198
A;Accession: UC5198
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-353 <UMB>
A;Residues: 1-353 <UMB>
C;Genetics:
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Molecule type: DNA
Molecule type: DNA
Molecule type: DNA
Molecule type: DNI
Molecule type: DNI
Molecule type: MIPROT: P08280; UNIPPARC: UPI0000133516; GB: X05691; NID: 945413; PIDN: CA; Cossa-references: UNIPROT: P08280; UNIPPAC: UNIPPORT: Molecule type mature protein, was confirmation to this sequence, including the amino end of the mature protein, was confirmation to the EMBL Data Library, March 1990
Molecule to the EMBL Data Library, March 1990
A; Description: Restriction polymorphism and nucleotide sequence substitutions in the rec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Description: plays an essential role in homologous recombination, in induction of the C; Superfamily: recombination protein recA C; Superfamily: recombination protein recA C; Keywords: ATP; DNA binding; DNA recombination; DNA repair; nucleotide binding; P-loop; F; 65-72/Region: nucleotide-binding motif A (P-loop) F; 139-144/Region: nucleotide-binding motif B F; 71/Binding site: ATP (Lys) #status predicted
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N.Alternate names: recombinase A
C.Species: Pseudomonas aeruginosa
C.Species: Pseudomonas aeruginosa
C.Species: Pseudomonas aeruginosa
C.Species: Pseudomonas aeruginosa
C.Species: Pseudomonas aeruginosa
C.Species: Pseudomonas aeruginosa
C.Species: Pseudomonas aeruginosa
R.Sano, Y.; Kageyama, M.
MOI. Kageyama, M.
MOI. Gent. 208, 412-419, 1987
A.Title: The sequence and function of the recA gene and its protein in Pseuch A.Reference number: S06265; MUID:88038334; PMID:2823059
27-Feb-1997 #text_change 09-Jul-2004
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recombination protein recA - Azotobacter vinelandii

NyAlternate names: recombinase A

NyAlternate names: recombinase A

NyAlternate names: recombinase A

CyBecies Azotobacter vinelandii

C;Date: 09-0ct-1992 #sequence_revision 09-0ct-1992 #text_change 09-Jul-2004

C;Accession: JN0321

R;Kenkatesh, T.V.; Das, H.K.

Gene 113, 47-53, 1992

A;Title: The Azotobacter vinelandii recA gene: sequence analysis and regulation of expinance number: JN0321; MUD:9225347; PMID:1563632

A;Title: The Azotobacter vinelandii recA gene: sequence analysis and regulation of expinanceule type: DNA

A;Reference number: JN0321

A;Accession: JN0321

A;Residues: 1-349 cKEN>

A;Residues: 1-349 cKEN>

A;Coss-references: UNIPROT:P29246; UNIPARC:UPI00001334CC

A;Note: the authors translated the codon GAC for residue 129 as Val and AAC for residue C;Genetics:

A;Gene: recA

C;Genetics:
A;Gene: recA

C;Genetics:
A;Gene: recA

C;Superfamily: recombination protein recA

C;Superfamily: recombination protein recA

C;Superfamily: recombination protein recA

C;Superfamily: recombination protein recA

C;Superfamily: recombination protein recA

C;Superfamily: recombination protein recA

C;Superfamily: nucleotide-binding motif A (P-loop)

F;139-144/Region: nucleotide-binding motif A

F;71/Binding site: ATP (Lys) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 VEIYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSQPDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEQALEICDALARSGAVDVIVVDSVAALTPKAEIEGEIGDSHMGLAARMMSQAMRKLAGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 KANAAKFLEDNPEVAAAVEKSIRDQLLAAPAS 332
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      301 KANAAKYLEDNPEIGSVLEKTIRDQLLA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: February 16, 2006, 01:24:56
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A;Residues: 313-346 <SAN2>
A;Residues: 313-346 <SAN2>
A;Residues: 313-346 <SAN2>
A;Residues: 313-346 <SAN2>
A;Rolecule type: DNA
A;Residues: 313-346 <SAN2>
A;Robote: sequence extracted from NCBI backbone (NCBIN:129317, NCBIP:129318)
B;Rryukov, V.M.; Zaitsev, E.N.; Kouzmin, N.P.; Bayev, A.A.
B;Rryukov, V.M.; Zaitsev, E.N.; Kouzmin, N.P.; Bayev, A.A.
A;Reference number: JN0304; MUID:91182156; PMID:2127886
A;Reference number: JN0304; MUID:91182156; PMID:2127886
A;Residues: 1-332, 'L',334-346 <KRY>
A;Residues: 1-332, 'L',334-346 <KRY>
A;Residues: 1-332, 'L',334-346 <KRY>
A;Residues: 1-332, 'L',334-346 <KRY>
A;Residues: 1-332, 'L',334-346 <KRY>
A;Residues: 1-32,  'L',3337; PMID:10984043
A;Reference number: Ag2950; MUID:2043337; PMID:10984043
A;Reference number: Ag2950; MUID:2043337; PMID:10984043
                                                        A;Molecule type: DNA
A;Residues: 1-346 <ZAI>
A;Cross-references: UNIPARC:UPI0000133516; EMBL:X52261; NID:g45383; PIDN:CAA36504.1; PID
                                                                                                                                                                           J. Bacteriol. 175, 2451-2454, 1993
A;Title: Role of the recA-related gene adjacent to the recA gene in Pseudomonas aerugind
A;Reference number: A49854; MUID:93224470; PMID:8468303
A;Accession: A49854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: UNIPARC:UPI0000133516; GB:AE004782; GB:AE004091; NID:g9949772; PIDN:
Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Description: plays an essential role in homologous recombination, in induction of the C; Superfamily: recombination protein recA
C; Superfamily: recombination protein recA
C; Superfamily: recombination bNA repair; nucleotide binding; P-loop; F; 65-72/Region: nucleotide-binding motif A (P-loop)
F; 139-144/Region: nucleotide-binding motif B
F; 71/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
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ive 42; Mismatches 42; Indels
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Best Local Similarity 74.4%
Matches 244; Conservative
A; Reference number: S10458
A; Accession: S10458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-346 <STO>
                                                                                                                                                                                                                                                                                                        A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: recA; PA3617
C;Function:
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Pebruary 16, 2006, 01:14:35 ; Search time 152 Seconds
(without alignments)
1554.947 Million cell updates/sec Run on:

US-10-733-782-1 1678 Perfect score:

1 AIDENKQKALAAALGQIEKQ.........AKEIEKKVRELLLSNPNSTP 335 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2166443 segs, 705528306 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

į		عد			SUMMARIES	
resurt No.	Score	Query	Length	DB	ID	ρ
-	1678	100.0	ຕ	7	RECA ECO57	P0a7g8 escherichia
7	1678	100.0	352	Н	RECA_ECOL6	POa7g7 escherichia
m	1678	100.0	352	Н	RECA_ECOLI	escheric
4	1678	100.0	352	Н	RECA SHIFL	
ß	1671	99.6	352	н	RECA_SHISO	shigella
9	1641		352	Н	RECA_SALTI	
7	1641	97.8	352	-	RECA_SALTY	P65977 salmonella
80	1641	97.8	353	7	Q57KU4_SALCH	
σ	1639	97.7	353	~	Q5PF15_SALPA	
10	1547	92.2	e	н	RECA PHOLL	Q7n7a6 photorhabdu
11	1537	91.6	e	Н	RECA_ERWCT	
12	1534	91.4	m	Н	RECA YERPE	
13	1534	91.4	m	٦	RECA_YERPS	
14	1532	91.3	М	Н	RECA_ENTAG	enterobac
15	1527	91.0	m	٦	RECA_SERMA	P17479 serratia ma
16	1524	90.8	358	ч	RECA_XENBV	P96185 xenorhabdus
11	1523	90.8	m	Н	RECA_SODGL	
18	1513	90.2	m	7	Q6Y131_9ENTR	primary
19	1504	89.6	m	Н	RECA_PROMI	P11406 proteus mir
20	1501	89.5	m	-1	RECA_ERWCA	
21	1501	89.5	m	н	RECA_SHEON	Q8ebs0 shewanella
22	1500	89.4	m	-	RECA_XENNE	
23	1486	88.6	m	-	RECA_PROVU	proteus
24	1437	85.6	m	-	RECA_VIBCH	
25	1429	85.2	m	-	RECA VIBPA	Q871r1 vibrio para
56	1418	84.5	m	-	RECA_VIBNA	vibrio
27	1418	84.5	349	Н	RECA_VIBVU	Q8dc51 vibrio vuln
28	1418	84.5	349	ч	RECA_VIBVY	Q7mhr4 vibrio vuln
53	_		4	~	Q5E7G6_VIBF1	9
30	1412.5	84.2	348	Н	RECA VIBAN	~
31	1404		352	г	RECA_PHOPR	Q61mu2 photobacter

PIR; D91073; D91073

0984r6 vibrio chol 09r2w9 vibrio chol 09r2w9 vibrio chol P95526 pasteurella P43705 haemophilus 04gwv2 haemophilus 09r9u2 pseudomonas 05gb0 mannheimia 065gb0 mannheimia 08d2w7 wiggleswort 09jrp9 actinobacil 09rny0 pasteurella 06ev36 pseudomonas 06ev36 pseudomonas
O984R6_VIBCH O9RZW9_VYBCH RECA_HAEIN O40WV2_HAEIN O40WV2_HAEIS RECA_PECL OSOUBB_IDILO RECA_AEESA RECA_AEESA RECA_MIGHR RECA_AUGHR RECA_ACTAC RE
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1400 1353 1332 1332 1326 1326 1319 1317 1288 1276
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ALIGNMENTS

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=015:147 | Sakai / RIMD 0509952 / EHEC;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara M., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Complete genome sequence of enterchemorrhagic Escherichia coli "Complete genome sequence of enterchemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Res. 8:11-22(2001).
-!- FUNCTION: Can catalyze the hydrolysis of ATP in the presence of single-stranded DNA, the ATP-dependent uptake of single-stranded DNA by duplex DNA, and the ATP-dependent hybridization of homologous single-stranded DNAs. It interacts with lexA causing its activation and leading to its autocatalytic cleavage (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WICLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN-0157-117 / ED1933 / ATCC 700927 / EHEC;
MEDLINE-21074935, PubMed=11206551; DOI=10.1038/35054089;
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Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
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Welch R.A., Germent Escherichia coli 0157:H7.";
Nature 409:529-533(2001).
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352 AA
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EMBL; BA000007; BAB36979.1; -; Genomic_DNA
PRT;
STANDARD;
RECA ECO57
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R PRINTS; PR00142; RECA; 1.

R SMART; SM00382; AAA; 1.

R TIGREAM; TIGRO2012; Ligrfam_recA; 1.

R PROSITE; PS00321; RECA_1; 1.

R PROSITE; PS0162; RECA_2; 1.

R PROSITE; PS0162; RECA_2; 1.

R PROSITE; PS0162; RECA_3; 1.

R PROSITE; PS0162; RECA_3; 1.

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STANDARD; PRT; 352 AA.
P0A7G7; P03017; P5347; P78213;
21-JUL-1986 (Rel. 01, Casted)
21-JUL-1986 (Rel. 01, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
RecA protein (Recombinase A).
RecA protein (Recombinase A).
Recherichia coli 06.
HAMAP; ME_00268; -; 1.
InterPro; IRR001559; RAA ATPase.
InterPro; IPR001553; RecĀ.
Pfam; PP00154; RecA; 1.
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NCBI_TaxID=217992;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                            causing
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
DNA by duplex DNA, and the ATP-dependent hybridization of homologous single-stranded DNAs. It interacts with lexA caus its activation and leading to its autocatalytic cleavage (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00142; RECA.
Probom; PD000229; RecA; 1.
SWART; SM00322; AAA; 1.
TIGRFAMS; TIGR02012; Ligrfam_recA; 1.
PROSITE; PS00321; RECA_1; 1.
PROSITE; PS500162; RECA_2; 1.
PROSITE; PS50162; RECA_3; 1.
ATP-binding; Complete proteome; DNA damage; DNA recombination; DNA repair; DNA-binding; Nucleocide-binding; SOS response.
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66 73 ATP (By similarity).
352 AA; 37842 MW; 989B02378EC4A402 CRC64;
                                                                                                                  similarity).
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POA765; PO3017; P26347; P79213;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
RecA protein (Recombinase A).
Name-recA; Synonymea-laxB, recH, rnmB, tif, umuB, zab;
OrderedLocusNames=b2699;
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100.0%; Pred. No. 5.4e-104;
ive 0; Mismatches 0;
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SUBCELLULAR LOCATION: Cytoplasmic (By simil SIMILARITY: Belongs to the reck family.
                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE016765; AAN81704.1; -; Genomic_DNA.
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InterPro; IRR0015593; AAA ATPABE.
InterPro; IPR001553; RecĀ.
Pfam; PF00154; RecA<sub>i</sub> 1.
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[6]
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NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Story R.M., Weber I.T., Steitz T.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bscherichia coli RecA protein.";
Eur. J. Biochem. 233:419-425(1995).
                                                                                                                                                                (3]
NUCLEOTIDE SEQUENCE.
MEDLINE=91109725; PubMed=2274037;
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                                                                                                      NUCLEOTIDE SEQUENCE,
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 NCBI_TaxID=562;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
STRUCTURE OF ATP-BINDING FOLD.

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-! FUNCTION: Can catalyze the hydrolysis of ATP in the presence of single-stranded DNA, the ATP-dependent uptake of single-stranded DNA, by the ATP-dependent hybridization of homologous single-stranded DNAs. It interacts with lexA causing its activation and leading to its autocatalytic cleavage.
                                                                                                                                                                                                                                                                                                                                                                                                            C. POAGG7:C1pp, NDExp=1; IntAct=EBI-370331, EBI-370625, P0A6G7:C1pp, NDExp=1; IntAct=EBI-370331, EBI-545265; P7488.dexs, NDExp=1; IntAct=EBI-370331, EBI-545265; P77488.dexs, NDExp=1; IntAct=EBI-370331, EBI-57063; P06138.fte2; NDExp=1; IntAct=EBI-370331, EBI-57063; P091097:9274, NDExp=1; IntAct=EBI-370331, EBI-57129; P0A6H5.halU; NDExp=1; IntAct=EBI-370331, EBI-547129; P0A8H7.metk, NDExp=1; IntAct=EBI-370331, EBI-546295; P0A8H7.metk, NDExp=1; IntAct=EBI-370331, EBI-547088; P09155:narG; NDExp=1; IntAct=EBI-370331, EBI-548080; P09155:narG; NDExp=1; IntAct=EBI-370331, EBI-548080; P05055:pnp; NDExp=1; IntAct=EBI-370331, EBI-548080; P05055:pnp; NDExp=1; IntAct=EBI-370331, EBI-557453; P36979:yrd; NDExp=1; IntAct=EBI-370331, EBI-557453; P36979:yrd; NDExp=1; IntAct=EBI-370331, EBI-557453; P36979:yrd; NDExp=1; IntAct=EBI-370331, EBI-557453; P36979:yrd; NDExp=1; IntAct=EBI-370331, EBI-557453; P36979:yrd; NDExp=1; IntAct=EBI-370331, EBI-557453; P36979:yrd; NDExp=1; IntAct=EBI-370331, EBI-557453; P36979:yrd; NDExp=1; IntAct=EBI-370331, EBI-55971; C-1:INDUCTION: In response to low temperature. Sensitive to temperature through changes in the linking number of the DNA.
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Direct protein sequencing; DNA damage; DNA recombination; DNA repair;
DNA-binding; Nucleotide-binding; SOS response.
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EMBL; U00096; AAC75741.1; -; Genomic_DNA.
EMBL; D90892; BAA16561.1; -; Genomic_DNA.
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ProDom; PD000229; RecA; 1.
SNART; SM00382; AAA; 1.
TIGREAMS; TIGRO2012; tigrfam_recA; 1.
PROSITE; PS00321; RECA 1; 1.
PROSITE; PS50162; RECA 2; 1.
PROSITE; PS50163; RECA 3; 1.
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1AA3; NWR; @=-.
1N03; EM; A/B/C/D/E/F/G=1-352.
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J; 1U94; X-ray; A=1-352.

J; 1U99; X-ray; A=1-352.

J; 1U99; X-ray; A=1-352.

J; IXMS; X-ray; A=1-352.

J; IXMS; X-ray; A=1-352.

J; IXMS; X-ray; Q=-.
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InterPro; IPR001559; AAA ATPase.
InterPro; IPR001553; RecA.
Pfam; PP00154; RecA.
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PRINTS; PR00142; RECA.
ProDom; PD000229; RecA; 1.
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100.0%; Pred. No. 5.4e-104;
ive 0; Mismatches 0;
D -> E (in Ref. 5).
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The Pack, SHIPL, STRUMBAN, 1987; 352 AA.

PRICE, SHIPL, SHIPL, TO TRANSAN, 198213; 1987; 1824.

DY 21-701-1986 (Red. 01, Leat sequence update)

DY 21-701-1986 (Red. 01, Leat sequence update)

DY 21-701-1986 (Red. 01, Leat sequence update)

DY SHIPLES (Red. 01, Leat sequence update)

Red. Proced. (Recombinase A.)

Red. Canc. Canc. (Red. Proced. 22,1356-1376(1990).

Red. Canc. Canc. (Red. 20, May A.)

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Red. Canc. Canc. (Red. 20, May A.)

Red. Canc. (Red. Red. 10, May A.)

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Enterobacteriaceae; Shigella.
NCBI_TaxID=624;
PROSITE; PS50163; RECA_3; 1.
ATP-binding; Complete proteome; DNA damage; DNA recombination; DNA repair; DNA-binding; Nucleotide-binding; SOS response.
INTT MET 0 0 By similarity.
NP BIND 66 73 ATP (By similarity).
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                                                                        100.0%; Score 1678; DB 1; Length 352; 100.0%; Pred. No. 5.4e-104; cive 0; Mismatches 0; Indels 0
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(Rel. 39, Last sequence update)
(Rel. 48, Last annotation update)
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HSSP; P03017; 2REB.
SMR; Q9ZFF6; 3-328.
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NUCLEOTIDE SEQUENCE [GENOMIC DNA]
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                                                                                           Matches 335; Conservative
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30-MAY-2000
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HAMAP; MF_00268; -; 1.

InterPro; IPR003593; AAA_ATPage.
InterPro; IPR001593; RecĀ.
InterPro; IPR001593; RecĀ.
InterPro; IPR001593; RecĀ.
InterPro; PR00142; RECA.
InterPro; PR00142; RECA.
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P65978; Q8XET0;
28-FRB-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
RecA protein (Recombinase A).
Name=recA; OrderedLocusNames=STY2950, t2730;
Salmonella typhi.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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66 73 ATP (By similarity).
352 AA; 37799 MW; EECS0231893AA40C CRC64;
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99.7%; Pred. No. 1.6e-103;
iive 0; Mismatches 1;
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Matches 334; Conservative
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                                      STATUS SEQUENCE [LARGE SCALE GENOMIC DNA].

STATUS TYS / ATCC 700931;

MEDLINE-22531367; PubMed=12644504;

MEDLINE-22531367; PubMed=12644504;

DOI=10.1128/JB.185.7.2330-2337.2003;

Burland V., Kodoyiani V., Schwartz D.C., Blattner F.R.; Rose D.J.,

Burland V., Kodoyiani V., Schwartz D.C., Blattner F.R.; and CT18.";

"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";

J. Bacteriol. 185:2330-2337(2003).

J. Bacteriol. 185:2330-2337(2003).

J. Bacteriol. 185:2330-2374 che hydrolysis of ATP in the presence of single-stranded DNA, the ATP-dependent uptake of single-stranded DNA, the ATP-dependent hybridization of homologous single-stranded DNAs. It interacts with lexA causing the activation and leading to its autocatalytic cleavage (By
                                                                                                                                                                                                                                                                                                                                                                                                                                             This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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ATP-binding; Complete proteome; DNA damage; DNA recombination; DNA repair; DNA-binding; Nucleotide-binding; SOS response.

INIT MET 0 0 ATP (BV similarity)
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352 AA; 37813 MW; F24E51CB9A31B818 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 97.8%; Score 1641; DB 1; Local Similarity 97.3%; Pred. No. 1.6e-101; Nes 326; Conservative 5; Mismatches 4;
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EMBL; AE016843; AAO70291.1; -; Genomic_DNA.
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PROSITE; PS00321; RECA 1; 1.
PROSITE; PS50162; RECA 2; 1.
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InterPro; IPR003593; AAA ATPase.
InterPro; IPR01553; RecĀ.
Pfam; PF00154; RecA; 1.
PKINTS; PR00142; RECA;
ProDom; PD000229; RecA; 1.
  Nature 413:848-852(2001)
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SMR; P65978; 3-328.
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;

"Complete genome sequence of Salmonella enterica serovar Typhimurium
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DR HAMAP; MC 00266; -; 1.

DR InterPro; IPR001553; RecĀ.

DR RINTS; PR00154; RecĀ.

DR PRINTS; PR00142; RecĀ.

DR PRINTS; PR00142; RecĀ.

DR SMART; SM00382; AAA; 1.

DR SMART; SM00382; ReCA.

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Enterobacteriaceae, Salmonella.
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352 AA; 37813 MW; F24E51CB9A31B818 CRC64;
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97.3%; Pred. No. 1.6e-101;
ive 5; Mismatches 4;
301 GKANATTWLKENPATAKEIEKRVRELLLSNQNATP 335
                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
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HSSP; P03017; 2REB.
SMR; P65977; 3-328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RecA protein (Recombinase A).
Name=recA, OrderedLocusNames=STM2829;
Salmonella typhimurium.
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STRAIN=ATCC 9150 / SARB42;

SY PUNICLEDIA SARB42;

SY PUNICLEDIA W., Sanderson K.E., Clifton S.W., Latreille P.,

BA MCIelland W., Sanderson K.E., Clifton S.W., Latreille P.,

BA MCIelland W., Sanderson K.E., Clifton S.W., Latreille P.,

BA Harkins C.R., Wang C., Nguyen C., Berging E.A., Elliott G.,

Kohlberg S., Strong C., Du F., Carter J., Kremizki C., Layman D.,

RA Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P.,

BA Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P.,

BA Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P.,

RADIS Spieth J., Wilson R.K.;

"Comparison of genome degradation in Paratyphi A and Typhi, human-RT estricted servovars of Salmonella enterica that cause typhoid.";

RAT Genet. 36:1268-1274 (2004).

BAR, Ogrelis, 4-2329.

BOS GO:000526; AAV78544.1; -; Genomic_DNA.

BAR, Ogrelis, 4-2329.

CO; GO:000526; F.RATP binding; IEA.

GO; GO:000586; F.DNA-dependent Arpase activity; IEA.

GO; GO:000166; F.Nucleotide binding; IEA.

GO; GO:000581; P.DNA recombination; IEA.

BO; GO:000581; P.DNA recombination; IEA.

BO; GO:000581; P.DNA repair; IEA.

BO; GO:000581; P.DNA repair; IEA.

BO; GO:000581; P.DNA repair; IEA.

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BO; GO:000581; P.DNA repair; IEA.

BO; GO:000581; P.DNA repair; IEA.

BO; GO:000581; P.DNA repair; IEA.
                                                                                                                                                                                                                                                                   181 NLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLDIRRIGAVKEGENVVGS
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Name=recA; OrderedLocusNames=SPA2687;
Salmonella paratyphi-a.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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SEQUENCE 353 AA; 37962 MW; AD15A0C48E7CF6FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QSPP15_SALPA PRELIMINARY; PRT; 353 AA.
QSPP15;
Q1-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
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97.0%; Pred. No. 2.2e-101;
tive 6; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 GKANATTWLKENPATAKEIEKRVRELLLSNQNATP 336
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ProDom; PD000229; RecA; 1.
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Best Local Similarity 97.0
Matches 325; Conservative
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Enterobacteriaceae; Salmonella.
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PubMed=15781495; DOI=10.1093/nar/gki297;
Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,
Wang H.-S., Lee Y.-S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DNA strand exchange and recombination protein with proteiase
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97.3%; Pred. No. 1.6e-101;
ive 5; Mismatches 4;
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Name=recA; OrderedLocusNames=SC2762;
Salmonella choleraesuis.
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Q57KU4;
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           IVEIYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPVYARKLGVDIDNLLCSQPD
                                                                                                                                                              ETRVKVVKNKIAAPFKQAEFQILYGEGINFYGELVDLGVKEKLIEKAGAWYSYKGEKIGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-22957627; PubMed=14528314; DOI=10.1038/nbt886; MEDLINE-22957627; PubMed=14528314; DOI=10.1038/nbt886; MEDLINE-22957627; PubMed E., Edward E., Chandler M., Charles J.-F., Taourit S., Bocs S., Bouranaw-Eude C., Chandler M., Charles J.-F., Dassa E., Derose R., Derzelle S., Freyssinet G., Gaudriault S., Medigue C., Lanois A., Powell K., Siguier P., Vincent R., Wingate V., Zouline M., Glaser P., Boemare N., Danchin A., Kunst F.; The genome sequence of the entomopathogenic bacterium Photorhabdus luminescens.";
AIDENKQKALAAALGQIEKQFGKGSIMRLGEDRSMDVETISTGSLSLDIALGAGGLPMGR
                                                61 IVEIYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSQPD
                                                                                                TGEQALEICDALARSGAVDVIVVDSVAALTPKABIEGEIGDSHMGLAARMMSQAMRKLAG
                                                                                                                                                 NLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLDIRRIGAVKEGENVVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nat. Biotechnol. 21:1307-1313(2003).

-!- FUNCTION: Can catalyze the hydrolysis of ATP in the presence of single-stranded DNA, the ATP-dependent uptake of single-stranded DNA by duplex DNA, and the ATP-dependent hybridization of homologous single-stranded DNAs. It interacts with lexA causing its activation and leading to its autocatalytic cleavage (By
                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
RecA protein (Recombinase A).
Name=recA; OrderedLocusNames=plu1249;
Photorbhabdus luminescens (Subsp. laumondii).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaces; Photorhabdus.
NCBI TaxID=141679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the recA family.
                                                                                                                                                                                                                                                    301 GKANATAWLKDNPETAKEIEKKVRELLLSNPNSTP 335
                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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HAMAR; MF 00268; -; 1.
InterPro; IPR001553; RecA.
Pfam; PF00154; RecA.
PRINTS; PR00142; RECA.
ProDom; PD000229; RecA; 1.
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10-MAY-2005 (Rel. 47, Last sequence update)
13-SEP-2005 (Rel. 48, Last amotation update)
RecA protein (Recombinase A).
Name=recA; OrderedLocusNames=ECA3369;
Erwinia carctovora (subsp. atroseptica) (Pectobacterium atrosepticum).
Bacteria, Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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STRAIN-SCRI 1043 / ATCC BAA-672;

PubMed=15263089; DOI=10.1073/pnas.0402424101;

PubMed=15263089; DOI=10.1073/pnas.0402424101;

PubMed=15263089; DOI=10.1073/pnas.0402424101;

PubMed=15263089; DOI=10.1073/pnas.040244101;

PubMed=15263089; DOI=10.1073/pnas.04024101;

Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Hungall K., Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K., Atkin R., Bason N., Brooker K., Chillingworth T., Clark K., Doggett J., Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H., Fraser A., Hance Z., Quail M.A., Sanders M., Walker D., Whitehead S., Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;

"Genome sequence of the enterobacterial phytopathogen Erwinia carotovora subsp. atroseptica and characterization of virulence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 AIDENKQKALAAALGQIEKQFGKGSIMRLGEDRSMDVETISTGSLSLDIALGAGGLPMGR
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-I- FUNCTION: Can catalyze the hydrolysis of ATP in the presence of single-stranded DNA, the ATP-dependent uptake of single-stranded DNA by duplex DNA, and the ATP-dependent hybridization of homologous single-stranded DNAs. It interacts with lexA causing its activation and leading to its autocatalytic cleavage (By
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PROSITE; PS00321; RECA_1; 1.
PROSITE; PS00321; RECA_2; 1.
PROSITE; PS50162; RECA_2; 1.
ATP-binding; Complete Proteome; DNA damage; DNA recombination; DNA repair; DNA-binding; Nucleotide-binding; SOS response.
NP BIND 67
ATP (BY similarity).
SEQUENCE 355 AA; 38381 MW; PD659ACED827AEF9 CRC64;
                                                                                                                                                                                                                                                                                      92.2%; Score 1547; DB 1; Length 355; 92.1%; Pred. No. 3.1e-95; ive 15; Mismatches 11; Indels
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SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
SIMILARITY: Belongs to the recA family.
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Matches 304; Conservative
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removed.
        This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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R HAMAP; MF 00268; 4-329.

R InterPro; IPR001553; Recā.

DR InterPro; IPR001553; Recā.

DR Pfam; PF00154; Recā.

DR PRON142; RECA.

DR PRON175; SM00342; RECA.

DR PROSITE; PS00321; Ligrfam_recA; 1.

DR PROSITE; PS00321; Ligrfam_recA; 1.

DR PROSITE; PS50162; RECA_1; 1.

DR PROSITE; PS50162; RECA_2; 1.

DR PROSITE; PS50163; RECA_2; 1.

DR PROSITE; PS50163; RECA_3; 1.

DR PROSITE; PS50163; RECA_3; 1.

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Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.
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28-FEB-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
RecA protein (Recombinase A).
Name=recA, OrderediocusNames=YPO3307, y0881, YPO379;
Yersinia pestis.
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                                                                                                                                                                     EMBL; BX950851; CAG76267.1; -; Genomic_DNA.
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Enterobacteriaceae, Yersinia.
WCBI_TaxID=632;
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Matches 304; Conservative
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STRAIN=231;
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MEDLINE=22137863; PubMed=12142430;
DOI=10.1128/JB184.16.4601-4611.2002;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
Petheston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
                              STRAIN=CO-92 / Biovar Orientalis,
MEDLINE=21470413; PubMed=11566360; DOI=10.1038/35097083;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Genome sequence of Fyersinia pestis, the causative agent of plague.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D., Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z., Jin L., Dai R., Chen P., Li S., Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P., Yang R., "Complete genome sequence of Yersinia pestis strain 91001, an isolate avirulent to humans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PURATION: 11:179-197(2004).

-!- FUNCTION: Can catalyze the hydrolysis of ATP in the presence of single-stranded DNA, the ATP-dependent uptake of single-stranded DNA, by duplex DNA, and the ATP-dependent hybridization of homologous single-stranded DNAs. It interacts with lexA causing its activation and leading to its autocatalytic cleavage.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
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TIGRFAMS; TIGR02012; tigrfam_recA; 1.
TIGRTE, PS00321; RECA_1; 1.
PROSITE; PS50062; RECA_2; 1.
PROSITE; PS50163; RECA_3; 1.
ATP-binding; Complete proteome; DNA damage; DNA recombination; DNA repair; DNA-binding; Nucleotide-binding; SOS response.
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ATP (By similarity)
H -> L (in Ref. 1).
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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EMBL; AJ41156; CAC92539.1; -; Genomic DNA.
EMBL; AB013691; AAM84465.1; -; Genomic_DNA.
EMBL; AB017128; AAS60652.1; -; Genomic_DNA.
PIR; AG0401; AG0401.
PIR; S37586; S37586.
HSSP; P03017; ZEEB.
SWR; P37858; 3-328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).
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PubMed=15368893;
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InterPro; IPR001559; RecA.
InterPro; IPR001553; RecA.
Pfam; PF00154; RecA.
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ProDom; PD000229; RecA; 1.
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BX936398; CAH20063.1; -; Genomic_DNA
         SMR; Q66E70; 4-329.
HAMAP: MF 00268; -: 1.
InterPro: IPR001559; AAA_ATPase.
InterPro: IPR001553; RecA.
Pfam: PF00154; RecA.
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P33037;
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13-SEP-2005
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Matches 305;
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                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                              RecA protein (Recombinase A).
NamearecA, OrderedLocusNames=YPTB0823;
Nessinia pseudotuberculosis.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                       91.4%; Score 1534; DB 1; Length 355; 91.9%; Pred. No. 2.3e-94;
                                                          Indele
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294 294 N -> Y (in Ref. 1).
315 315 I -> N (in Ref. 1).
355 AA; 37755 MW; F800D2D1AD32AB81 CRC64;
                                                             13;
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NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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10-WAY-2005 (Rel. 47, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
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                                                          14; Mismatches
                                                             Conservative
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Matches 305; Conserv
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Submitted (JAN-1993) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Can catalyze the hydrolysis of ATP in the presence of
single-stranded DNA, the ATP-dependent uptake of single-stranded
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea.
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                                                                                                    PROSITE; PS00321; RECA_1; 1.
PROSITE; PS00321; RECA_2; 1.
PROSITE; PS50162; RECA_2; 1.
ATP-binding; Complete Protecome; DNA damage; DNA recombination; DNA repair; DNA-binding; Nucleotide-binding; SOS response.
NP BIND
SEQUENCE 356 AA; 37914 MW; DICOD90F58C8642B CRC64;
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                                                                                                                                                                                                                                                                                                            Length 356;
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                                                                                                                                                                                                                                                                                                                  DB 1;
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91.9%; Pred. No. 2.3e-94;
tive 14; Mismatches 13
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PRINTS; PR00142; RECA.
ProDom; PD000229; RECA; 1.
SMART; SM00382; AAA; 1.
TIGRPAMs; TIGR02012; tigrfam_recA; 1.
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PRODOM; PR001229; RECA; 1.

SMART; SM00382; AAA; 1.

TIGRFAMS; TIGR02012; tigrfam_recA; 1.

PROSITE; PS00321; RECA_1; 1.

PROSITE; PS0162; RECA_2; 1.

PROSITE; PS0162; RECA_2; 1.

ATP_binding; DNA damage; DNA recombination; DNA repair; DNA-binding;
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FP (By similarity).
960F1F2698CAC46B CRC64;
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MEDLINE-90094239; PubMed=2152908;
Ball T.K., Wasmuth C.R., Braunagel S.C., Benedik M.J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 1532; DB 1; 
; Pred. No. 3.1e-94; 
15; Mismatches 11
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16-OCT-2001 (Rel. 40, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Name=recA protein (Recombinase A).
                                                                                                                                                    EMBL; L03291; AAA91766.1; -; Genomic_DNA.
PIR; S31481; S31481.
HSSP; P03017; 2REB.
SMR; P33037; 3-328.
HAWAP; MF 00268; -; 1.
InterPro; IPR003593; AAA ATPase.
Pfam; PF00154; RecA; 1.
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GKANSCNYLKENPKVAAELDKKLRDMLLS 329
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Bacteria; Proteobacteria; Gam
Enterobacteriaceae; Serratia.
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                    recă.";
J. Bacteriol. 172:342-349(1990).
J. Bacteriol. 172:342-349(1990).
J. Bacteriol. 172:342-349(1990).
J. PUNCTION: Can catalyze the hydrolysis of ATP in the presence of single-stranded DNA, the ATP-dependent uptake of single-stranded DNA, and the ATP-dependent hybridization of homologous single-strand DNA. It interacts with lexA causing its activation and leading to its autocatalytic cleavage.
J. SUBCELLUTAR LOCATION: Cytoplasmic (By similarity).
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PROSITE; PS00321; RECA_2; 1.
PROSITE; PS50162; RECA_2; 1.
ATP-binding; DNA damage; DNA recombination; DNA repair; DNA-binding; Nucleotide-binding; SOS response.
INIT_MET 0 0 0 By similarity; NPT-BIND 66 73 ATP (By similarity).
"Expression of Serratia marcescens extracellular proteins requires
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66 73 ATP (By similarity).
353 AA; 37778 MW; A97369360970F814 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M22935; AAA26567.1; -; Genomic_DNA.
HSSP; P03017; 2REB.
SMR; P17479; 3-328.
HAMAP; MF 00268; -; 1.
InterPro; IPR003593; RecĀ.
PINCEPPO; IPR001553; RecĀ.
PRINTS; PR00142; RECA.
PRODOM; PD0000229; RecA; 1.
SWART; SM00382; AAA; 1.
TIGRFAMS; TIGR2012; tigrfam_recA; 1.
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Sequence 7, Appl
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US-09-626-410-19

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US-09-516-695B-10

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Maximum Match 100%
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US-09-126-99

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US-09-126-051-9

US-09-126-051-11

US-09-126-051-12

US-09-626-410-12

US-09-626-343-12

US-09-126-051-13

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ALIGNMENTS

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Length 353;
Sequence 5510473
; Sequence 5510473
; Patent No. 5510473
; GENERAL INFORMATION:
APPLICANT: Camernio-Otero, Rafael D.
TITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STREET: 620 Newport Center Drive 16th Floor
STREET: CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMERICAN CAMER
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COUNTRY: USA
ZIP: 92660
COMPUTER PADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DAY
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,831
FILING DATE: 19930726
CLASSIFICATION: 435
ATTOMEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: NIH066.001A
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 353 amino acids TYPE: amino acid STRANDEDNESS: single
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GENERAL INFORMATION:
APPLICANT: DEL CARDATE, STEPHEN
APPLICANT: DEL CARDATE, WILLEN
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APPLICANT: MINSHULL, JEREN
APPLICANT: MINSHULL, JEREN
APPLICANT: STEWMEN, VENKITSWARN
APPLICANT: GASTLE, LINDA
APPLICANT: STEWMER, CLAUS M.
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ETRVKVVKNKIAAPFKQAEPQILYGEGINPYGELVDLGVKEKLIEKAGAWYSYKGEKIGQ 300
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Best Local Similarity 100.0%; Pred. No. 2.6e-167;
Matches 335; Conservative 0; Mismatches 0;
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                                                                                                     301 GKANATAWLKDNPETAKEIEKKVRELLLSNPNSTP 335
                                                                                                                              RESULT 4
US-09-626-410-14
Sequence 14, Application US/09626410
Patent No. 6297862
GENERAL INFORMATION:
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ORGANISM: Escherichia coli
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APPLICANT: MINSHUL, JEREMY
APPLICANT: MINSHUL, JEREMY
APPLICANT: MINSHUL, JEREMY
APPLICANT: SUBLAMANIA, PHILLIP
APPLICANT: SUBLAMANIA, PHILLIP
APPLICANT: CASTLE, LINDA
APPLICANT: KREBBER, CLAUS M.
APPLICANT: SEQUENCE RECOMBINATION
TITLE OF INVENTION: SEQUENCE RECOMBINATION
FILE REFERENCE: 0.2-0.20.720US
CURRENT APPLICATION NUMBER: US/09/626,410
CURRENT APPLICATION NUMBER: 09/116,188
PRIOR APPLICATION NUMBER: 09/116,188
PRIOR PLING DATE: 0.7-15-1998
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN OF: 2.0
SEG ID NO 7
LENGTH: 3.58
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US-09-626-410-7
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US-09-626-410-7
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APPLICANT: TOBIN, MATTHEW
APPLICANT: STEMMER, WILLEM P.C.
APPLICANT: NESS, JON E.
APPLICANT: NESS, JON E.
APPLICANT: MINSHULL, JEREMY
APPLICANT: SUBRAMANIA, VENKITSWARAN
APPLICANT: SUBRAMANIA, VENKITSWARAN
APPLICANT: CASTLE, LINDA
APPLICANT: KREBBER, CLAUS M.
APPLICANT: KREBBER, CLAUS M.
APPLICANT: RESS, STEVE
TITLE OF INVENTION: SEQUENCE RECOMBINATION
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         TITLE OF INVENTION: SEQUENCE RECOMBINATION FILE REFERENCE: 02-020720US
                                     CURRENT APPLICATION NUMBER: US/09/116,188
CURRENT FILLING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
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CURRENT APPLICATION NUMBER: US/09/116,188
CURRENT FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
LENGTH: 358
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                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-116-188-7
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US-09-116-188-9
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                                                                                                                                                                 LENGTH: 358
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                                     APPLICANT: STEMMER, WILLEM P.C.
APPLICANT: STEMMER, WILLEM P.C.
APPLICANT: NESS, JON E.
APPLICANT: NESS, JON E.
APPLICANT: PATTEN, PHILLIP
APPLICANT: SUBRAMANIA, VERKITSWARAN
APPLICANT: CASTLE, LINDA
APPLICANT: KREBER, CLAUS M.
APPLICANT: REBERS, STEVE
TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
TITLE OF INVENTION: SEQUENCE RECOMBINATION
FILE REFERENCE: 02-020720US
CURRENT APPLICATION NUMBER: US/09/626,410
FILE REFERENCE: 02-020720US
CURRENT FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 09/116,188
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: SUBRAWANIA, VENKITSWARAN
APPLICANT: CASTLE, LINDA
APPLICANT: KEBBER,
APPLICANT: REBERS, STEVE
TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 IVEIYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSQPD
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Patent No. 6326204
GENERAL INFORMATION:
APPLICANT: DEL CARDAYRE, STEPHEN
APPLICANT: STEMMEN, WILLEM P.C.
APPLICANT: NESS, JON E.
APPLICANT: MINSHULL, JEREMY
DEL CARDAYRE, STEPHEN
TOBIN, MATTHEW
STEMMER, WILLEM P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 14
LENGTH: 358
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US-09-116-188-7
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Sequence 7, Application US/09626047;
Sequence 7, Application US/09626047;
Batent No. 6335198
GENERAL INFORMATION:
APPLICANT: DEL CARDAYRE, STEPHEN
APPLICANT: TOBIN, MATTHEW
APPLICANT: STEMMER, WILLEM P.C.
APPLICANT: SUBRAMMANIA, VENEMY
APPLICANT: PATTEN, PHILLIP
APPLICANT: PATTEN, PHILLIP
APPLICANT: RESS, ONN E.
APPLICANT: RESBER, CLANS M.
APPLICANT: RESERRE, CLANS M.
APPLICANT: RASS, STEVE
TITLE OF INVENTION: SEQUENCE RECOMBINATION
FILE REFERENCE: 02-020720US
CURRENT APPLICATION NUMBER: US/09/626,047
CURRENT FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 09/116,188
PRIOR APPLICATION NUMBER: 09/116,188
PRIOR FILING DATE: 2000-07-26
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247 ETRYKVYRNKIAAPFKQAEFQILYGEGINFYGELVDLGVKEKLIEKAGAWYSYKGEKIGQ 306
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100.0%; Score 1678; DB 2; Length 358;
Best Local Similarity 100.0%; Pred. No. 2.6e-167;
Matches 335; Conservative 0; Mismatches 0; Indels 0
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SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Escherichia coli
US-09-626-047-7
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US-09-626-047-7
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US-09-626-047-9
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Sequence 14, Application US/09116188

Patent No. 6326204

GENERAL INFORMATION:
APPLICANT: DEL CARDAYRE, STEPHEN
APPLICANT: STERMER, WILLEM P.C.
APPLICANT: STERMER, WILLEM P.C.
APPLICANT: SUBRAMANIA, VENKITSWARN
APPLICANT: BUSS, JON E.
APPLICANT: RUBSALALI, DEREMY
APPLICANT: RUBSAMIA, VENKITSWARN
APPLICANT: GASTLE, LINDA
APPLICANT: GASTLE, LINDA
APPLICANT: GASTLE, LINDA
APPLICANT: GASTLE, LINDA
APPLICANT: GASTLE, LINDA
APPLICANT: GASTLE, LINDA
APPLICANT: GASTLE, LINDA
APPLICANT: GASTLE, LINDA
APPLICANT: GASTLE, LINDA
APPLICANT: GASTLE, LINDA
APPLICANT: GASTLE, LINDA
APPLICANT: BASS, STEVE
CAPRENTION: SEVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
TITLE OF INVENTION: SEVOLUTION
CURRENT APPLICATION NUMBER: US/09/116,188
CURRENT FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VET. 2.0
SECO ID NO 18
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                                   7 AIDENKQKALAAALGQIEKQFGKGSIMRLGEDRSMDVETISTGSLSLDIALGAGGLFWGR
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; Pred. No. 2.6e-167;
0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 335; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 14
LENGTH: 358
TYPE: PRT
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Query Match 100.0%; Score 1678; DB 2; Best Local Similarity 100.0%; Pred. No. 2.6e-167; Matches 335; Conservative 0; Mismatches 0;
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                            PILE REFERENCE: 02-020720US
CURRENT APPLICATION NUMBER: US/09/626,047
CURRENT FILING DATE: 2000-07-26
PRIOR PILING DATE: 09/116,188
PRIOR PILING DATE: 07-15-1998
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SERIOR NO. 14
LENGTH: 358
              TITLE OF INVENTION: SEQUENCE RECOMBINATION
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CURRENT FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 09/116,188
PRIOR FILING DATE: 07-15-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: TOBIN, MATTHEW
APPLICANT: TOBIN, MATTHEW
APPLICANT: STEWMER, WILLEM P.C.
APPLICANT: STEWNER, WILLEM P.C.
APPLICANT: MINSHULL, JEREMY
APPLICANT: PATTEN, PHILLIP
APPLICANT: SUBRAMANIA, VENKITSWARN
APPLICANT: GASTLE, LINDA
APPLICANT: KREBBER, CLAUS M.
APPLICANT: BASS, STEVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09626343
Patent No. 6352859
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGIH: 358
TYPE: PRT
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                                                                                                                            APPLICANT: STEMMER, WILLEM P.C.
APPLICANT: NESS, JON E.
APPLICANT: NESS, JON E.
APPLICANT: NISHULL, JERENY
APPLICANT: PINTSHULL,
APPLICANT: PATTEN, PHILLIP
APPLICANT: SUBRAMANIA, VENKITSWARAN
APPLICANT: SUBRAMANIA, VENKITSWARAN
APPLICANT: KREBBER, CLAUS M.
APPLICANT: REBBER, CLAUS M.
APPLICANT: REBBER, CLAUS M.
APPLICANT: REBBER, CLAUS M.
APPLICANT: REBBER, CLAUS M.
APPLICANT: RESERVER, STEVE
ITTLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
ITTLE OF INVENTION: EVOLUTION NUMBER: US/09/626,047
CURRENT APPLICATION NUMBER: US/09/116,188
PRIOR FILING DATE: 07-15-1998
RRIOR FILING DATE: 07-15-1998
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 9
FRACTION 13-58
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APPLICANT: MINSHULL, JEREMY
APPLICANT: PATTEN, PHILLIP
APPLICANT: CASTLE, LINDA
APPLICANT: CASTLE, LINDA
APPLICANT: CASTLE, LINDA
APPLICANT: RREBBER, CLAUS M.
APPLICANT: RREBBER, CLAUS M.
TITLE OF INVENTION: BASS, STEVE
TITLE OF INVENTION: BVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
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100.0%; Score 1678; DB 2; Length 358;
Best Local Similarity 100.0%; Pred. No. 2.6e-167;
Matches 335; Conservative 0; Mismatches 0; Indels 0
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                                                  GENERAL INFORMATION:
APPLICANT: DEL CARDATER, STEPHEN
APPLICANT: DEL CARDATER, STEPHEN
APPLICANT: STEMMER, WILLEM P.C.
APPLICANT: NESS, JON E.
APPLICANT: MINSHULL, JEREMY
APPLICANT: BATTEN, PHILLIP
APPLICANT: SUBRAMANIA, VENKITSWARAN
APPLICANT: GASTLE, LINDA
APPLICANT: GASTLE, LINDA
APPLICANT: REBBER, CLAUS M.
APPLICANT: BASS, STEVE
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Patent No. 6335198
Application US/09626047
335198
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APPLICANT: DEL CARDAYRE, STEPHEN
APPLICANT: TOBIN, MATTHEW
APPLICANT: STEMMER, WILLEM P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Bscherichia coli
US-09-626-047-9
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US-09-626-047-14
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TYPE: PRT
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APPLICANT:
APPLICANT:
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APPLICANT: KREBBER, CLAUS M.
APPLICANT: BASS, STEVE
TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
TITLE OF INVENTION: SEQUENCE RECOMBINATION
FILE REFERENCE: 02-020727US
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PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: consensus
OTHER INFORMATION: e. coli sequence
15.03-626-047-14
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STERMER, WILLEM P.C.

APPLICANT: NESS, JON E.

APPLICANT: PATTEN, PILLIP P.C.

APPLICANT: PATTEN, PILLIP P.C.

APPLICANT: SUBRAWNIA, VENKITSWARAN

APPLICANT: CASTLE, LINDA

APPLICANT: KREBER, CLAUS M.

APPLICANT: REBER, CLAUS M.

APPLICANT: SEQUENCE RECOMBINATION

TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE

TITLE OF INVENTION: SEQUENCE RECOMBINATION

FILE REFERENCE: 02-02072/US

CURRENT FILING DATE: 07-05-05

PRIOR FILING DATE: 07-15-1998

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PALENTIN Ver. 2.0

SEQ ID NO 14

LENGTH: 358
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100.0%; Score 1678; DB 2; Length 358;
Best Local Similarity 100.0%; Pred. No. 2.6e-167;
Matches 335; Conservative 0; Mismatches 0; Indels 0
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TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
TITLE OF INVENTION: SEQUENCE RECOMBINATION
FILE REPERENCE: 02-020727US
CURRENT APPLICATION NUMBER: US/09/626,343
PRIOR APPLICATION NUMBER: 09/116,188
PRIOR APPLICATION NUMBER: 09/116,188
PRIOR FILING DATE: 07-15-1998
NUMBER OF SEQ ID NOS: 14
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2.6e-167;
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100.0%; Pred. No. 2.6e-167;
vative 0; Mismatches 0;
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100.0%; Score 1678;
Best Local Similarity 100.0%; Pred. No. 2.6
Matches 335; Conservative 0; Mismatches
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APPLICANT: DEL CARDAYER, STEPHEN
APPLICANT: TOBIN, MATTHEM
APPLICANT: STEMMER, WILLEM P.C.
APPLICANT: NESS, JON E.
APPLICANT: NESS, JON E.
APPLICANT: SUBRAMANIA, VENKITSWARAN
APPLICANT: SUBRAMANIA, VENKITSWARAN
APPLICANT: CASTLE, LINDA
APPLICANT: BASS, STEVE
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Patent No. 6352859
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SEQ ID NO 9
LENGTH: 358
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; ORGANISM: Escherichia coli
US-09-626-343-7
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Best Local Similarity
Matches 335; Conserv
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APPLICANT: STEMMER, WILLEM P.C.
APPLICANT: NESS, JON E.
APPLICANT: MINSHULL, JEREMY
APPLICANT: PATTEN, PHILLIP
APPLICANT: SUBRAMANIAN, VENKITESWATAN
APPLICANT: CASTLE, LINDA A.
APPLICANT: KREBBER, CLAUS M.
                                                TOBIN, MATTHEW STEMMER, WILLEM P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-354-922-10
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                                                                                                                                                                        Sequence 8, Application US/09354922

Sequence 8, Application US/09354922

Patent No. 6379964

GENERAL INFORMATION:

APPLICANT: DEL CARDAYRE, STEPHEN

APPLICANT: STEWMER, WILLEM P.C.

APPLICANT: STEWMER, WILLEM P.C.

APPLICANT: BASS, JON E.

APPLICANT: PATTEN, FHILLIP

APPLICANT: SUBRAMANIAN, VENKITESWATAN

APPLICANT: SUBRAMANIAN, VENKITESWATAN

APPLICANT: CASTLE, LINDA A.

APPLICANT: CASTLE, LINDA A.

APPLICANT: CASTLE, LINDA A.

APPLICANT: COX, TONY

APPLICANT: COX, TONY

APPLICANT: VING-XIN

APPLICANT: VING-XIN

APPLICANT: VING-XIN

APPLICANT: SUBRAMA, GJALT

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APPLICANT: SUBRAMA, GJALT

APPLICANT: STERORENCE: 02-02730UB

TITLE OF INVENTION: SEQUENCE RECOMBINATION

TITLE OF INVENTION: SEQUENCE: 02-02730UB

TITLE OF INVENTION NUMBER: US/09/354,922

CURRENT FILING DATE: 1999-07-15

SOUFWANDE: DEFANCT: V.-.

SOUFWANDE: DEFANCT: V.-.

SOUFWANDE: DEFANCE: V.-.
247 ETRVKVVKOKIAAPFKQAEFQILYGEGINFYGELVDLGVKEKLIEKAGAWYSYKGEKIGQ 306
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                                           301 GKANATAWLKDNPETAKEIEKKVRELLLSNPNSTP 335
                                                                  307 GKANATAWLKDNPETAKEIEKKVRELLLSNPNSTP 341
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ORGANISM: Escherichia coli
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US-09-354-922-10
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APPLICANT: ANEABLE, CLAUS M.
APPLICANT: ANEABLE, VING-XIN
APPLICANT: ZHANG, YING-XIN
APPLICANT: COX, TONY
APPLICANT: HUISMAN, GJALT
APPLICANT: YUAN, LING
APPLICANT: YUAN, LING
APPLICANT: AFFHOLTER, JOSEPH A.
TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE TITLE OF INVENTION: SEQUENCE RECOMBINATION
CURRENT APPLICATION NUMBER: US/09/354,922
CURRENT FILING DATE: 1999-07-15
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100.0%; Score 1678; DB 2;
Best Local Similarity 100.0%; Pred. No. 2.6e-167;
Matches 335; Conservative 0; Mismatches 0;
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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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US-10-282-122A-75948
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US-10-282-122A-758953
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US-10-282-122A-6695
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US-10-282-122A-69902
US-10-282-122A-69902
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US-10-282-122A-61949
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                                                                                                                                                                                                                                                                                                                                                                                                                                 1867569 seqs, 417829326 residues
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Maximum Match 100%
Listing first 45 summaries
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Sequence 6597.7 A
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Sequence 49452, A
Sequence 51342, A
Sequence 51342, A
Sequence 51342, A
Sequence 51363, A
Sequence 51953, A
Sequence 51953, A
Sequence 51953, A
Sequence 61898, A
Sequence 71934, A
Sequence 71834, A
Sequence 7631, A
Sequence 7631, A
Sequence 7631, A
Sequence 7631, A
Sequence 7631, A
Sequence 7631, A
Sequence 7631, A
Sequence 7631, A
Sequence 7634, A
Sequence 7631, A
       US-10-282-122A-65975
US-10-282-122A-65031
US-10-282-122A-47848
US-10-282-122A-49452
US-10-282-122A-51342
US-10-282-122A-51342
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US-10-282-122A-1654
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100.0%; Pred. No. 4.2e-152;
tive 0; Mismatches 0;
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Sequence 1, Application US/1073782
Publication No. US20040157248A1
GENERAL INFORMATION:
APPLICANT: Cox, Michael
APPLICANT: Lusetti, Shelley
APPLICANT: Lusetti, Shelley
APPLICANT: Eggler, Aimee
FILE REFERENCE: 960296, 99501
CURRENT APPLICATION NUMBER: US/10/733, 782
CURRENT PILLNG DATE: 2003-12-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.2
SOFTWARE: 2355
LENGTH: 235
                                                                                                                                                                                                                                                                                                            TYPE: PRT
; ORGANISM: Escherichia coli
US-10-733-782-1
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Matches 335; Conservative
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GENERAL INVENTATION:
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Alane, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Wall, Daniel
APPLICANT: Carr, Grant
APPLICANT: Yamamoco, Robert
APPLICANT: Yamamoco, Robert
APPLICANT: Yamamoco, Robert
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100.0%; Pred. No. 4.5e-152;
tive 0; Mismatches 0;
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Sequence 5, Application US/1073782
Publication No. US20040157248A1
GENERAL INFORMATION:
APPLICANT: Cox, Michael
APPLICANT: Lusetti, Shelley
APPLICANT: Lusetti, Shelley
APPLICANT: Eggler, Aimee
FILE REFERENCE: 960296 99501
CURRENT APPLICATION NUMBER: US/10/733,782
CURRENT APPLICATION NUMBER: 2003-12-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SERNGTH: 352
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US-10-733-782-5
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Matches 335; Conservative
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US-10-282-122A-43319
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PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-22
PRIOR PLING DATE: 2000-11-22
PRIOR PLING DATE: 2001-12-22
PRIOR PLING DATE: 2001-02-09
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PRIOR PLING DATE: 2000-03-06
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100.0%; Pred. No. 4.5e-152;
tive 0; Mismatches 0;
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Jelion No. US20030148309A1

JELICANT: DEL CARDAYRE, STEPHEN

APPLICANT: TOBIN, WATTHEW
APPLICANT: STEWMER, WILLEM P.C.
APPLICANT: STEWMER, WILLEM P.C.
APPLICANT: NESS, JON E.
APPLICANT: NESS, JON E.
PPLICANT: BATTHEN, PHILLIP
PLICANT: SUBRAMANIAN, VENKITESWATAN
'LICANT: CASTLE, LINDA A.
ICANT: KREBBER, CLAUS M.
CANT: EARNG, YING-XIN
'THUISMAN, GJALT
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Best Local Similarity 100.
Matches 335; Conservative
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US-10-194-686-8
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SOFTWARE: Patentin Ver. 2.0
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APPLICANT: AFFHOLTER, JOSEPH A.
TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE FILE REFRENCE: 02-020730US
FILE REFERENCE: 02-020730US
CURRENT APPLICATION NUMBER: US/10/194,686
CURRENT FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: US/09/354,922
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 15
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APPLICANT: COX, TONY
APPLICANT: HUISMAN, GJALT
APPLICANT: YOAN, LING
APPLICANT: YOAN, LING
APPLICANT: AFHOLTER, JOSEPH A.
TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
FILE REFERENCE: 02-020730US
CURRENT APPLICATION NUMBER: US/10/194,686
PRIOR PLING DATE: 1999-07-11
PRIOR PLING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 15
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Publication No. US20030148309A1
GENERAL INFORMATION:
APPLICANT: DEL CARDAYRE, STEPHEN
APPLICANT: TOBIN, MATTHEW
APPLICANT: STEMMER, WILLEM P.C.
APPLICANT: MINSHULL, JEREMY
APPLICANT: PATTEN, PHILLIP
APPLICANT: BATTEN, PHILLIP
APPLICANT: SUBRAMANIAN, VENKITESWATAN
APPLICANT: KREBBER, CLAUS M.
APPLICANT: KREBBER, CLAUS M.
APPLICANT: GASTLE, LINDA A.
APPLICANT: GASTLE, LINDA A.
APPLICANT: GASTLE, LINDA A.
APPLICANT: GASTLE, LINDA A.
APPLICANT: REBBER, CLAUS M.
APPLICANT: STANG, YING-XIN
                                                                                                                                                                                                                                                                       ; ORGANISM: Bscherichia coli
US-10-194-686-8
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TYPE: PRT
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61 IVBIYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSQPD 120
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APPLICANT: AFFROLTER, JOSEPH A.
TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
TITLE OF INVENTION: SEQUENCE RECOMBINATION
FILE REFERENCE: 02-020730US
CURRENT APPLICATION NUMBER: US/10/194,686
CURRENT PILING DATE: 1999-07-11
PRIOR PILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTI VET. 2.0
SOFTWARE: PATENTI VET. 2.0
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OTHER INFORMATION: e. coli sequence
US-10-194-686-15
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                                                                                                                               Length 358;
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                                                                                                                               100.0%; Score 1678; DB 4;
100.0%; Pred. No. 4.6e-152;
iive 0; Mismatches 0;
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APPLICANT: TOBIN, MATTHEM
APPLICANT: STEMMER, WILLEM P.C.
APPLICANT: NESS, JON E.
APPLICANT: MINSHULL, JEREMY
APPLICANT: SUBBAMANIAN, VENKITESWATAN
APPLICANT: CASTLE, LINDA A.
APPLICANT: KREBBER, CLAUS M.
APPLICANT: RASS, STEVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15, Application US/10194686; Publication No. US20030148309A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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COX, TONY
HUISMAN, GJALT
                        TYPE: PRT
ORGANISM: Escherichia coli
                                                                                                                                                        Best Local Similarity 100.
Matches 335; Conservative
                                                                          US-10-194-686-10
LENGTH: 358
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US-10-194-686-12
; Sequence 12, Application US/10194686
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APPLICANT: TOBLN, MATTHEW
APPLICANT: STEMMER, WILLEM P.C.
APPLICANT: STEMMER, WILLEM P.C.
APPLICANT: MINSHULL, DEREMY
APPLICANT: BATTEN, PHILLIP
APPLICANT: GRATLE, LINDA A.
APPLICANT: GREBER, CLAUS M.
APPLICANT: GREBER, CLAUS M.
APPLICANT: GRATL, LINDA A.
APPLICANT: GRATL, LINDA A.
APPLICANT: GRAS, STEVE
APPLICANT: GRAS, STEVE
APPLICANT: GRAN, ILNG
APPLICANT: HULSMAN, GJALT
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APPLICANT: HULSMAN, LING
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APPLICANT: 
                                                                                                                                                                          ; Sequence 9, Application US/10194686; Publication No. US20030148309A1; GENERAL INFORMATION:
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ORGANISM: Escherichia coli
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Length 358;
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Pred. No. 1e-151;
1; Mismatches 0; Indels
                                                      0; Indels
  Query Match
100.0%; Score 1678; DB 4;
Best Local Similarity 100.0%; Pred. No. 4.6e-152;
Matches 335; Conservative 0; Mismatches 0;
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Publication No. US20040157248A1
GRNERAL INFORMATION:
APPLICANT: Cox, Michael
APPLICANT: Lusetti, Shelley
APPLICANT: Bggler, Aimee
TITLE OF INVENTION: RecA Mutents
FILE REFERENCE: 960296, 99501
CURRENT APPLICATION NUMBER: US/10/733,782
CURRENT PILING DATE: 2003-12-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 335
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Best Local Similarity 99.7%;
Matches 334; Conservative
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US-10-733-782-3
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US-10-733-782-3
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APPLICANT: ARBEDBAF, CLANDS N.
APPLICANT: ENAS, STEVE
APPLICANT: COX, TONY
APPLICANT: COX, TONY
APPLICANT: VHOWAN, GJALT
APPLICANT: YORN, LING
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANTON: SEQUENCE RECOMBINATION
TITLE OF INVENTION: SEQUENCE RECOMBINATION
FILE REPERBANCE: 02-02073008
CURRENT FILING DATE: 202-07-11
PRIOR FILING DATE: 1999-07-15
NUMBER: OF SEQUENCE OS: 15
NUMBER: OS: 15
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Best Local Similarity 99.4%; Pred. No. 1.4e-151;
Matches 333; Conservative 1; Mismatches 1;
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NESS, JON E.
MINSHULL, JEREMY
PATTEN, PHILLIP
SUBRAMANIAN, VENKITESWATAN
CASTLE, LINDA A.
KREBBER, CLAUS M.
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*** KREBER, CLAUS M.

*** CLICANT: BASS, STEVE

*** APPLICANT: ZHANG, YING-XIN

*** APPLICANT: ZHANG, YING-XIN

*** APPLICANT: HUISMAN, GJALT

*** APPLICANT: HUISMAN, GJALT

*** APPLICANT: HUISMAN, GJALT

*** APPLICANT: WING-XIN

*** APPLICANT: WING-XIN

*** APPLICANT: WING-XIN

*** APPLICANT: WING-XIN

*** APPLICANT: WING-XIN

*** APPLICANT: WING-XIN

*** TITLE OF INVENTION: ENDUER RECOMBINATION

*** FILE REFERENCE: 02-020730US

*** CURRENT APPLICATION NUMBER: US/10/194,686

*** CURRENT APPLICATION NUMBER: US/09/354,922

*** PRIOR PILING DATE: 1999-07-15

*** SOFTWARE: PatentIn Ver: 2.0

*** SEQ ID NO 13

*** LENGTH: 358

*** TYPE: POPT
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APPLICANT: HUISWAN, GJALT
APPLICANT: YUAN, LING
APPLICANT: YUAN, LING
APPLICANT: AFFHOLITER, JOSEPH A.
TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
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Pred. No. 2.5e-150;
1; Mismatches 3;
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APPLICANT: TOBIN, MATHEW
APPLICANT: STEMMER, WILLEM P.C.
APPLICANT: NESS, JON B.
APPLICANT: MINSHULL, JERENY
APPLICANT: PATTEN, PHILLIP
APPLICANT: SUBRAMANIAN, VEKITESWATAN
APPLICANT: CASTLE, LINDA A.
APPLICANT: KREBEER, CLAUS M.
APPLICANT: KREBEER, CLAUS M.
APPLICANT: STANG, YING-XIN
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Publication No. US20030148309A1
GENERAL INFORMATION:
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Best Local Similarity 98.8%;
Matches 331; Conservative
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, ORGANISM: Escherichia coli
US-10-194-686-13
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US-10-194-686-11
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APPLICANT: TOBIN, MATTHEM P.C.
APPLICANT: STEMMER, WILLEM P.C.
APPLICANT: STEMMER, WILLEM P.C.
APPLICANT: NISS, JON E.
APPLICANT: BATTEN, PHILLIP
APPLICANT: CASTLE, LINDA A.
APPLICANT: CASTLE, LINDA A.
APPLICANT: CASTLE, LINDA A.
APPLICANT: CASTLE, LINDA A.
APPLICANT: CASTLE, LINDA A.
APPLICANT: COX, TONY
APPLICANT: COX, TONY
APPLICANT: THOUSAND, GUALT
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99.7%; Score 1673; DB 4;
Best Local Similarity 99.4%; Pred. No. 1.4e-151;
Matches 333; Conservative 2; Mismatches 0;
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US-10-194-686-13
Sequence 13, Application US/10194686
Publication No. US20030148309A1
GENERAL INFORMATION:
APPLICANT: DEL CARDAYRE, STEPHEN
APPLICANT: TOBIN MATTHEM
APPLICANT: STEMMER, WILLEM P.C.
APPLICANT: MESS, JON E.
APPLICANT: MINSHULL, JEREMY
APPLICANT: MINSHULL, JEREMY
APPLICANT: SUBRAMANIAN, VENKITESWATAN
APPLICANT: SUBRAMANIAN, VENKITESWATAN
                                                                                                                                                                                                                     APPLICANT: DEL CARDAYRE, STEPHEN
                                                                                                                                                       Publication No. US20030148309A1
GENERAL INFORMATION:
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; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 12
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Escherichia coli
:US-10-194-686-12
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Pred. No. 3.1e-150;
; TITLE OF INVENTION: SEQUENCE RECOMBINATION
FILE REFERENCE: 02-020730US
CURRENT APPLICATION NUMBER: US/10/194,686
CURRENT FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: US/09/354,922
PRIOR FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 11
LENGTH: 358
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Best Local Similarity 99.1%;
Matches 332; Conservative
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, ORGANISM: Escherichia coli
US-10-194-686-11
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US-10-282-122A-75948
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121 TGEQALEICDALARSGAVDVIVVDSVAALTPKAEIEGEIGDSHMGLAARMMSQAMRKLAG 180
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APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2000-12-25
PRIOR FILING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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Pred. No. 1.6e-148;
5; Mismatches 4;
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
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; Sequence 59525, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Yeavick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Foreyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Salmonella typhi
US-10-282-122A-75948
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Best Local Similarity 97.3<sup>3</sup>
Matches 326; Conservative
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61 IVEIYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSQPD 120
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                                        CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
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Sequence 78524, Application US/10282122A
Sequence 78524, Application US/10282122A
Publication No. US20040029129A1
SERERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Amalone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Zyskind, Judith
APPLICANT: Mall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Enterobacter cloacae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-282-122A-55632
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PRIOR FILING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR PAPLICATION NUMBER: 60/207,727
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
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PRIOR PLING DATE: 2001-02-09
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PRIOR PLING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-06
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-03-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 7.7e-146;
8; Mismatches 7;
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangeu
APPLICANT: Aselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Obleen, Kari
APPLICANT: Carlos
APPLICANT: Carlos
APPLICANT: Aselbeck, Judith
APPLICANT: Carlos
APPLICANT: Year, Carlos
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
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95.5%;
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Best Local Similarity 95.55
Matches 320; Conservative
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APPLICANT: Trawick, John
APPLICANT: Carr Grant
APPLICANT: Yamanoto, Robert
APPLICANT: Yamanoto, Robert
APPLICANT: You, H.
TITLE OP INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITAR.034A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
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PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,939
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/225,538
PRIOR APPLICATION NUMBER: 60/225,538
PRIOR PILING DATE: 2000-11-22-20
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-16
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91.4%; Score 1534; DB 4; Length 356;
Best Local Similarity 91.9%; Pred. No. 3e-138;
Matches 305; Conservative 14; Mismatches 13; Indels
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| GKANASNYLKENPAIAAELDKKLREMLLNGGN 333
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US-10-282-122A-78524
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Sequence 4766, App
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Sequence 3092, App
Sequence 3092, App
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10599, A
3626, Ap
50, Appl
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4148, Ap
132, App
14, Appl
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Sequence 9, Appli
                                                                                                                   February 16, 2006, 01:40:35; Search time 10.5 Seconds (without alignments) 453.421 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USOS_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USOS_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USOS_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USIS_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USII_NEW_PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-078-66-11427
US-11-098-686-110861
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US-10-467-657-3092
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US-10-467-657-3066
US-10-467-657-3626
US-10-467-657-3626
US-10-467-657-4148
US-11-082-389-132
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US-11-082-389-132
US-11-114-922-6
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US-11-1082-389-124
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Maximum Match 100%
Listing first 45 summaries
                                                                              protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Gaps

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DB 6; Length 375;

72.3%; Score 1212.5; DB 6; Length 69.0%; Pred. No. 4e-86; iive 52; Mismatches 48; Indels

Query Match
Best Local Similarity 69.0
Matches 225; Conservative

CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR PILING DATE: 2003-08-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 4766
LENGTH: 375

TYPE: PRT ORGANISM: Neisseria gonorrhoeae

US-10-467-657-4766

9 87 61 IVEIYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSQPD 120

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7420, Ap 10, Appl

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28 MSDDKSKALAAALAQIEKSFGKGAIMKMDGSQQEENLEVISTGSLGLDLALGVGGLPRGR

2 IDENKOKALAAALGQIEKOFGKGSIMRL-GEDRSMDVETISTGSLSLDIALGAGGLPMGR

TGEQALEICDALARSGAVDVIVVDSVAALTPKAEIEGEIGDSHMGLAARMMSQAMRKLAG 180

NLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLDIRRIGAVKEGENVVGS 240

ETRVKVVKNKIAAPFKQAEFQILYGEGINFYGELVDLGVKEKLIEKAGAWYSYKGEKIGQ 300

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56	93.5	5.6	069	7	US-11-212-443-171	Sequence 171, App
27	93.5	9.9	710	۲	-212-4	equence 30. A
28	92.5	•	687	7	-443	
53	92.5		710	7	US-11-212-443-28	Sequence 28. Appl
30	92	5.5	302	9	US-10-793-626-2798	
31	92	•	376	7	US-11-213-368-6	
32	92	•	650	9	US-10-878-556A-110	11
33	92		806	7	-	
34	92	•	908	7	∹	1118.
35	92	•	806	7	US-11-079-900-1	1. Apr
36	91.5	•	569	9	US-10-506-443A-35	35
37	90.5	5.4	548	9	32	326
38	90.5	5.4	718	6	US-11-074-176-306	306,
39	90.5	5.4	723	7	US-11-074-176-18	18.
40	90	5.4	885	9	US-10-467-657-2302	
41	89.5	5.3	419	ø	-10-979-821-4	
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43	68		423		-11-070-080-	, ,
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45	88.5	5.3	633	7	US-11-232-406A-20	Sequence 20, Appl
					ALIGNMENTS	
RESULT 1 IIS-10-467-657-4766	7-657-4	766				
; Sequen	ce 4766	Applic	ation 1	JS/	Sequence 4766, Application US/10467657	
, Public	Publication No.	o. US20(US20050260581A1	31A	1	
; GENERA	GENERAL INFORMATION:	RMATION:	5			
APPLICANT		FONTANA Maria	4	4		
APPLICANT		PIZZA Mariagrazi	iagraz	g		
; APPLI	APPLICANT: M	MASIGNANI Vega	Vega			
; APPLI	APPLICANT: MONACI Elisabetta	DNACI E	lisabeti	æ		
, TITLE	OF INV	ENTION:	GONOCO	Š	TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS	IDS
, FILE RE		FERENCE:		:		

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US-11-098-686-10861
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                                                SEQ ID NO 11427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 VKVVKNKIAAPFKQAEFQILYGEGINFYGELVDLGVKEKLIEKAGAWYSYKGEKIGQGKA 303
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Publication No. US20060024696A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
FILE REPERENCE: 09531-128001
FILE REPERENCE: 09531-128001
CURRENT APPLICATION NUMBER: US/11/098,686
CURRENT FILING DATE: 2005-04-04
PRIOR PELLING DATE: 2003-10-01
PRIOR PLLING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: US 60/416,395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 ENKOKALAAALGQIEKQFGKGSIMRLGEDRSMDVETISTGSLSLDIALGAGGLPMGRIVE
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                                                                                                                     Sequence 296, Application US/11074176

| Sequence 296, Application US/11074176
| Publication No. US20050250135A1
| GENERAL INFORMATION:
| APPLICANT: Russell, William M. APPLICANT: Russell, William M. APPLICANT: Altermann, Eric APPLICANT: Altermann, Eric APPLICANT: APPLICANT: APPLICANT: APPLICANT: Peril, Andrea Azcarate TITLE OF INVENTION: Nucleic Acid Sequences Encoding TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore; FILE OF INVENTION: Stress-Related Proteins and Uses Therefore; FILE REPERBENCE: 5051-694
| CURRENT FILING DATE: 2005-03-07
| PRIOR PAPLICATION NUMBER: 60/551,161
| PRIOR PAPLICATION NUMBER: 60/551,161
| RROR FILING DATE: 2004-03-08
| NUMBER OF SEQ ID NOS: 381
| SEQ ID NO 296
| LENGTH: 363
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301 GKANATAWLKDNPETAKEIEKKVREL 326
                    || :|:::|:
NAKKYLEEHPDIYQKVQEQVRQ 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Lactobacillus acidophilus US-11-074-176-296
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QVIAAAQREGKTCAFIDAEHALDPIYAR--KLGVDIDNLLCSQPDTGEQALEICDALARS 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kapur, Vivek and Gebhart, Connie J.
TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
TITLE OF INVENTION: PROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
TITLE OF INVENTION: PROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
FILE REFERENCE: 05531-128001
CURRENT APPLICATION NUMBER: US/11/098,686
CURRENT FILING DATE: 2005-04-04
PRIOR PLILING DATE: 2003-10-01
PRIOR FILING DATE: 2003-10-04
PRIOR FILING DATE: 2003-10-04
NUMBER OF SEQ ID NOS: 11433
SOFTWARE: PSELEGQ for Windows Version 4.0
SEQ ID NO 10861
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                                                                                                                                                                                                                                                                                                                                                       EDSRREALKTALDTIERKFGGGAVMKLSDDVHVKVAVIPTGSIGLDLALGIGGIPRGRVT
                                                                                                                                                                                                                                                                                                                                                                                                                              ELYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSQPDTG
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                                                                                                                                                                                                                        57.8%; Score 970.5; DB 7; Length 355; 57.3%; Pred. No. 1.5e-67; tive 64; Mismatches 76; Indels 1
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PRIOR FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 11433
SOFTWARE: FastSEQ for Windows Version 4.0
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; Publication No. US20060024696A1
; GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SegWin99, version 1.04
TOWN 16-1
                                                                                                                                   ORGANISM: Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6400
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nes 65; Conserv
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                                                                                                                                                          US-10-467-657-206
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Best Local S
Matches 65
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  136 GAVDVIVVDSVAALTPKAEIEGEIGDSHMGLAARMMSQAMRKLAGNL----KQSNTLLIF 191
                                :||:|:||
----VSQ-VRAVATELVBACKQGKTTVIF 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85 REGKTCAFIDAEHALDPIYARKLGVDID----NLLCSQPDTGEQALEICDALARSGAVDV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 IVVDSVAALTPKAEIEGEIGDSHMGLAARMMSQAMRKLAGNL----KQSNTLLIFINQIR 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MKIGVMFGNPETTT-----GGNALKFYASVRLDIRRIGAVKEGENVVGSETRVKVV 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 SIMRLGEDRSMDVETISTGSLSLDIALGAGGLPMGRIVEIYGPESSGKTTLTLQVIAAAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217 TKDGAIAG-PRVLEHMVDTVLYFEGDQHSNYRMIRAIKNRFGAANELGVFAMTENGLKGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6; Length 459;
                                                                                                                                                                                                                                      Sequence 3092, Application US/10467657

Publication No. US20050260581A1

GENERAL INFORMATION:

APPLICANT: CHIRON SpA

APPLICANT: PIZZA Mariagrazia

APPLICANT: PIZZA Mariagrazia

APPLICANT: MASIGNAI Vega

APPLICANT: MONACI Elisabetta

TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

FILE REPERENCE:

CURRENT APPLICATION NUMBER: US/10/467,657

CURRENT FILING DATE: 2003-08-11

PRIOR APPLICATION NUMBER: GB-0103424.8

PRIOR APPLICATION NUMBER: GB-0103424.8

NUMBER OF SEQ ID NOS: 9218

SOFTWARE: SEQWIN99, VETRION 1.04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 206, Application US/10467657
; Sequence 206, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: MASIGNAII Vega
; APPLICANT: MASIGNAII Vega
; APPLICANT: MONANCI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFRERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 6.6%; Score 111.5; l Similarity 22.0%; Pred. No. 0.2: 65; Conservative 44; Mismatches
                           160 EAPDLLLIDSVQTLT-SSNAEGLPGN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Neisseria gonorrhoeae
                                                                                                                                 209 iGHV-TKDĞTLAĞ 220
                                                                                       192 INQIRMKIGVMFG 204
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Best Local Similarity
Matches 65; Conserv
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US-10-467-657-206
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57 PMGRIVBIYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPI----YARKLGVDID 112
                                                                                                                                                                                                                                                                                        201 PDGNLIVIAARPSMGKTVLAENIARFALKQGKAVHFQSYEMSAVELARRGMAAECNIPMQ 260
                                                                                                                                                                                                                                                                                                                                                      146
                                                                                                                                                                                                                                                                                                                                                                                                         261 NİKTGNLTQSDYANMPIYVSQAKEWKPDVNCDLLNVDELCFLAKEKKLTTGLDLLVVDHL 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 AALTPKA--EIEGEIGDSHMGLAARMMSQAMRKLAGNLKQSNTLLIFINQIRMKIGVMFG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261 NLKTGNLTQSDYANMPIYVSQAKEWKFDVNCDLLNVDELCFLAKEKKLTTGLDLLVVDHL 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 PDGNLIVIAARPSMGKTVLAENIARFALKOGKAVHPQSYEMSAVELARRGMAAECNIPMQ 260
                                                                                                                                                                                                                                                                                                                                                   113 NL-----ARSGAVDTGEQALE----ICDAL------ARSGAVDVIVVDSV
                                                                                                                    1 AIDENKOKALAAALGQ-IEKQFGKGSIMRLGEDRSMDVET--ISTGSLSLDIALG-AGGL
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0.36;
hes 91; Indels
     DB 6; Length 453;
                                                           91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6400, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: FORTANA Maria Rita
APPLICANT: FOZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MANACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 NPETITGGNALKFYASVR---LDIRRIGAVKEGENVV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.5%; Score 109; DB 6
Best Local Similarity 23.5%; Pred. No. 0.36;
Matches 65; Conservative 43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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23.5%; Pred. No. 0
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CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 6410
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US-10-467-657-3626
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LENGTH: 925
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Publication No. US20060024696A1

GENERAL INFORMATION:

APPLICANT: Kapur, Vivek and Gebhart, Connie J.

TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES

TITLE OF INVENTION: FROM LANGONIA INTRACELLULARIS AND METHODS OF USING

TITLE OF INVENTION: PROM LANGONIA INTRACELLULARIS AND METHODS OF USING

TITLE OF INVENTION: PROM LANGONIA INTRACELLULARIS AND METHODS OF USING

TITLE OF ILLING DATE: 2005-04-04

PRIOR APPLICATION NUMBER: US 60/416,395

PRIOR APPLICATION NUMBER: US 60/416,395

PRIOR FILING DATE: 2002-10-04

NUMBER OF FILING DATE: 2002-110-04

NUMBER OF SEQ ID NOS: 11433

SOFTWARE: FRACESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             332 QEISEISRSLKSLAKEINIPVVALSQLNRKL-----EDRTDKRPQLS------DLRES 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 ELEKRF------ERKEQVIGITIGYNRLD-KLTAGLQPSDLIIVAARP-SMGKTAF 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 TLQV-IAAAQREGKTCAFIDAEHALDPIYARKL----GVDIDNLLCS--QPDTGEQALEI 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 CDALARSGAVDVIVVDSVAALTP-----KAEIEGEI------GDSHMGLAA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         276 ADVLGQA----PIFIDDTPALSPLELRARTRRLKIESDVGLVVIDYLQLMRGNKRTDSRE 331
                          16 QIEKQFGKGSIMRLGEDRSMDVETISTGSLSLDIALGAGGLPMGRIVEIYGPESSGKTTL 75
147 AALTPKA--EIEGEIGDSHMGLAARMMSQAMRKLAGNLKQSNTLLIFINQIRMKIGVMFG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 RMMSQAMRKLAGNLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLDIRRI
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; Publication No. US20050260581A1
; GENERAL INFORMATION:
    APPLICANT: CHIRON SpA
; APPLICANT: FONTAM Maria Rita
APPLICANT: FONTAM Maria Rita
APPLICANT: MASIGNAIN 'Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.2%; Score 104; DB 7; Length 454; 22.0%; Pred. No. 0.86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94; Indels
                                                                                                                    205 NPETTTGGNALKFYASVR---LDIRRIGAVKEGENVV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45; Mismatches
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Best Local Similarity 22.0%
Matches 55; Conservative
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APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Gregor
APPLICANT: Schroder, Gregor
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
TITLE OF INVENTION NUMBER: US /10/454,437
CURRENT APPLICATION NUMBER: US 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 ----YARKLGVDIDNL-----LCSQPDTGEQALE----ICDAL----- 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 ARRGMAAECHIPMQNLKTGNLTQSDYANMPIYVSQAKEWKFDVNCDLLNVDELCFLAKEK 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307 KLITGLDLLVVDHL-HIMPRAGRDEVAELGN-----ISRRLKNLAABL---NIPVV 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | : : | | | : : | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | : : | | : : | | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : : | : : : | : : : | : : : | : : : | : : | : : | : : | : : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
6.1%; Score 102; DB 6; Length 453;
Best Local Similarity 23.4%; Pred. No. 1.2;
Matches 68; Conservative 42; Mismatches 87; Indels
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US-10-454-437-50
Selemence 50, Application US/10454437
Publication No. US20050277115A1
GENERAL INFORMATION:
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SEGWIN99, VERSION 1.04
SEQ ID NO 3626
                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
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248

301

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263 -----KAGVTLRDPARFDLRGRLKHGQDVVIDVNVVIEGEVELGDNVEIGANC---VIK 313
                                                                                                                                                                                                                                                                                                       137 AVDVIVVDSVAALTPKAEIEGEIGDSHMGLAARMMSQAMRKLAG-----NLKQSNTLLIF 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 ---DIDNLLCSQPDTGEQALEICDALAR-----SGAVDVIVVDSVAALTPKAEIEGEIG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218 YASVRLDIR-----RIGAVKEG---ENVVGS-ETRVKVVKNKIAAPPKQAEFQILYGEG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192 INQIRMKIGVMFGNPETTTGGNALKFYASVRLDIRRI--GAVKEGENV-VGSETRVKVVK
                                                                                                                                                                                                                                                             249 N-KIAAPFKQAEFQILYGEGI---NPYGELVDLGVKEKLIEK--AGAWYSYKGEKIGQG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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APPLICANT: CHIRON SpA
APPLICANT: FOXTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REPERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR APPLICATION NUMBER: GB-0103424.8
NUMBER OF SEQ ID NOS: 9218
SOTWARE: Seqwing9, version 1.04
SEQ ID NO 4148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 5.9%; Score 99; DB 6; Length 291; 1 Similarity 23.7%; Pred. No. 1.1; 63; Conservative 44; Mismatches 83; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4148, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
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GENERAL INFORMATION: APPLICANT: Pompejus, Markus
APPLICANT: Pompejus, Markus
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; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4148
                                                                    220 VADGİKVRPV-----
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374 KANHLTYIGD 383
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Best Local Similarity
Matches 63; Conserv
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US-10-467-657-4148
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US-11-082-389-132
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                                                                                                                                                                                                                                                                                                55 GLPMGRIVEIYGPESSG-----KTTLTL----QVIAAAQREGKTCAFIDAEHALDPIYAR 105
                                                                                                                                                                                                                                                                                                                                                                                                                  106 KLGVD------IDNLLCSQPDTGEQALEICDALARSGAVDVIVVDSVAALTPKAE 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 DKEIERIMQVLSRRTKANPVLIGEPGVGKTAV------VEGLALDIVNGKVPETL 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 IEGEIGDSHMG-LAARM-----MSQAMRKLAGNLKQSNTLLIFINQIRMKIGVMFGNPET 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :| :: | :: | :: | 320 AIDAASLLKPKLARGELQTIGATTLDEYRKHIEKDAALERRREGPV--QVPEPSVDLTVEI 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ::: |: :||||: |
TLVIXGDVPLIDVETLETLLEAAGNEVGLLTDVPADPAGL--GRIIR----DGSGSVTAI 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 LYG------EGINFYGELVDLGVKEK-----LIEKAGAWYSYKGEKIG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNILCSQPDTGEQALEICDALARSG 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 TIGGNALKFYASVRLDIRRIGAV-----KEGENVVGSETRVKVVKNKIAAPFKQAEFQI
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                                                                                                                                                                                               Gaps
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                                                                                                                        Query Match 6.0%; Score 101; DB 6; Length 925; Best Local Similarity 19.4%; Pred. No. 3.9; Matches 75; Conservative 67; Mismatches 125; Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 802, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MONBER: 21004067,657
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT PILING DATE: 2003-08-11
PRIOR PILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTMANE: SeqMin99, version 1.04
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; Pred. No. 1.8;
40; Mismatches 128; Indels
                                                                                                                                                                                                                                                      14 LGQIEKQFGKGS--IMRLGED----RSMDVETIS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Corynebacterium glutamicum
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US-10-467-657-802
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Best Local Similarity 25.8*
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
US-10-467-657-802
                                                          US-10-454-437-50
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APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Calder, Oskar
APPLICANT: Haberhauer, Gregor
ITILE OF INVENTION: CORYNBBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
ITILE OF INVENTION: INVOLUED IN MEMBRANE
TITLE OF INVENTION: TRANSPORT
FILE REFERENCE: BGI-131CPCN
CURRENT APPLICATION NUMBER: US 09/603024
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR PILING DATE: 2000-06-23
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 ------GLAARWMSQAMRKLAGNLKQSNTLLIFINQIRMKIGVMFGNPETTTGGN 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 PPALTLIFDRHPIAALLCYPAARYLMGSM-TPQAVLAPVALI-------PPTLPGTN 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 NLLCSQP-----DTGEQALEICDALARSGAVDVIVVDSVAALTPKAEIEGEIGDSHM-
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APPLICANT: Bertino, Joseph R.

TITLE OF INVENTION: Method for Modulating the Production of a Selected
TITLE OF INVENTION: Protein In
TITLE OF INVENTION: Vivo
FILE REFERENCE: MSK.P-053
CURRENT APPLICATION NUMBER: US/11/213,368
CURRENT APPLICATION NUMBER: US/10/421,285
PRIOR APPLICATION NUMBER: US/10/421,285
PRIOR FILING DATE: 2003-04-22
PRIOR FILING DATE: 2002-04-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.2
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23.6%; Pred. No. 2.3;
tive 30; Mismatches 80
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Publication No. US20050244935A1
GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
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Best Local Similarity 23.6%
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: herpes virus US-11-213-368-14
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US-11-082-389-130
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LENGTH: 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 IYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSQPDTGE 123
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                                          APPLICANT: SchInder, Hallwid
APPLICANT: SchInder, Hallwid
APPLICANT: Abberhauer, Gregor
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNBEACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: TRANSPORT
TITLE OF INVENTION: TRANSPORT
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TITLE OF INVENTION: TRANSPORT
TITLE OF INVENTION: UNMER: US 09/603024
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-07-09
PRIOR PELING DATE: 1999-07-01
PRIOR PELING DATE: 1999-07-01
PRIOR PELING DATE: 1999-07-01
PRIOR PELING DATE: 1999-07-01
PRIOR PELING DATE: 1999-07-01
PRIOR PELING DATE: 1999-07-08
PRIOR PELING DATE: 1999-07-08
PRIOR PELING DATE: 1999-07-09
PRIOR PELING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 1993134.5
PRIOR APPLICATION NUMBER: DE 1993134.5
PRIOR PELING DATE: 1999-07-09
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                                Schroder, Hartwig
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LENGTH: 365
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Sequence 14, Application US/11213368; Publication No. US20060003936A1; GENERAL INFORMATION; APPLICANT: MayerKuckuk, Phillip; APPLICANT: Banerjee, Debabrata

US-11-213-368-14

Gaps

62;

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80; Gaps 12;
                                                                                                                                                                                                                                                                                                                            306 ------TVAVTGGVQMVFQDPQSSLNPRMKIKDIVAEPLIGWNA------AB 345
                                                                                                                                                                                                                                                                                                                                                                                      64 IYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSQPDTGE 123
                                                                                                                                                                                                                                                                                                                                                                                                                               ------KPTTG- 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          346 KTTRVAEVITQVGLSPDVLDRXPHEFSGGQ-----RQRISIARALAIKPA--ILLADEP 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 VKVVKNKIAAPFKQAEFQILYGEGINFYGELVDLGVKEKLIEKAGAWYSYKGEKIGQGKA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          398 VSALDVSVRKQVLDLLQQLVEEYGITLVFVSHDLAVVRHLC--TTVWVMEQGRVLEQGPI 455
                                                                                                                                                                                                                                                                                                       7 QKALAAAL---GQIEKQFGKGSIMRLGEDRSMDVETISTGSLSLDIALGAGGLPMGRIVE 63
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19941379.7
PRIOR PILING DATE: 1999-08-31
Remaining Prior Application data removed - See File Wrapper or PALM.
Remaining Prior Application data removed - See File Wrapper or PALM.
SEQ ID NO 130
LENGTH: 479
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-11-082-389-130
                                                                                                                                                                                                                         Query Match 5.8%; Score 97; DB 7; Length 479; Best Local Similarity 20.5%; Pred. No. 3.2; Matches 67; Conservative 54; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 NATAWLKDNPET--AKEIEKKVRELLL 328
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Search completed: February 16, 2006, 01:45:01 Job time : 11.5 secs

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Pebruary 16, 2006, 01:14:10 ; Search time 132 Seconds
(without alignments)
1115.090 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	crip	Adr16430 E. coli R	Adr16428 E. coli R	Adr16432 E. coli w	Abul5395 Protein e	-	Aay68829 Amino aci		Adq87822 E. coli r	ω.	Aay68831 Amino aci	Aaw64213 New minsh	Aay68828 Amino aci		Adq87826 E. coli r	Aaw64215 Hyperreco	Aaw64214 Hyperreco	Aaw64217 Hyperreco	Aaw64218 Hyperreco	Aay68832 Amino aci	Adq87827 E. coli r		Adq87825 E. coli r	Aaw64216 Hyperreco	Abu48024 Protein e
SUMMARIES	OI ;	ADR16430	ADR16428	ADR16432	ABU15395	AAY68827	AAY68829	ADQ87824	ADQ87822	ADQ87821	AAY68831	AAW64213	AAY68828	ADQ87823	ADQ87826	AAW64215	AAW64214	AAW64217	AAW64218	AAY68832	ADQ87827	AAY68830	ADQ87825	AAW64216	ABU48024
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Abu31601	Abo63433	Abu27708	Abm67793	Abu50600	Abu40669	Ad£05150	Abu44971	Abu49151	Abu39491	Abu30311	Abo72381	Abu38581	Abu40018	Abu16844	Ada36276	Abu41878	Ad105025	Abu35468	Adr21929	Abu33125
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25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

LT 1 5430 ADR16430 standard; protein; 335 AA.
ADR16430;
04-NOV-2004 (first entry)
B. coli RecA mutant protein #2.
RecA; DNA binding protein; ssDNA binding protein; SSB; DNA strand exchange reaction; site-specific cleavage; mutant;
Escherichia coli.
Key Location/Qualifiers Misc-difference 18
/note= "Wild-type Glu substituted by Lys"

ALIGNMENTS

mutein.

US2004157248-A1. 12-AUG-2004.

11-DEC-2003; 2003US-00733782.

12-DEC-2002; 2002US-0432758P. (COXM/) COX M M. (LUSE/) LUSETTI S L. (EGGL/) EGGLER A L. (HARU/) HARUTA N.

Eggler AL, Haruta N; Cox MM, Lusetti SL,

WPI; 2004-580265/56. N-PSDB; ADR16431.

New RecA mutant proteins comprising a single mutation or a double mutation, useful for catalyzing homologous DNA pairing and DNA strand exchange reactions in an in vitro or in vivo environment.

Claim 13; SEQ ID NO 3; 34pp; English.

The invention relates to an isolated RecA mutant protein, where the protein is either a single mutant RecA protein comprising a deletion of amino acid residues from the carboxyl terminus, or a double mutant RecA protein comprising a deletion of amino acid residues from the carboxyl

12-DEC-2002; 2002US-0432758P.

COXM/) LUSE/)

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terminus and an amino acid change from a glutamate to a basic amino acid.

The invention also relates to a polynucleotide sequence that encodes the secA mutant protein, a method of catalysing an in vitro homologous DNA pairing and DNA strand exchange reactions comprising providing an amount of the RecA mutant protein and a method of increasing recombination efficiency of homologous DNA pairing and DNA strand exchange reactions in a cell comprising supplying to the cell an amount of the RecA mutant protein as comprises an enhanced capacity to displace a DNA binding protein as compared to wild-type RecA. The DNA binding protein is the ssDNA binding protein from Escherichia coli (SSB). It also comprises enhanced binding to DNA during a DNA strand exchange reaction as compared to wild-type RecA. The composition and methods are useful for catalysing homologous DNA pairing and DNA strand exchange reactions in an in vitro or in vivo environment. These may be used in promoting in vitro alterations of genes to permit the rapid construction of desired gene mutants for industrial and pharmaceutical purposes. The mutant protein may also be used in targeting the site-specific cleavage of small and large DNAs, or as a basis for the design and construction of tiny electronic circuits based on DNA. This sequence represents a RecA mutant protein of the invention.
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Sequence 335 AA;

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                                                                                                                                          61 IVEIYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSQPD
                                                                                                                                                                                                                                  121 TGEQALEICDALARSGAVDVIVVDSVAALTPKAEIEGEIGDSHWGLAARWMSQAMRKLAG
                                                                                                                                                                                                                                                                                                       181 NLKQSNT'LLIFINQIRMKIGVMPGNPETTTGGNALKFYASVRLDIRRIGAVKEGENVVGS
                                                                    1 AIDENKQKALAAALGQIEKQFGKGSIMRLGEDRSMDVKTISTGSLSLDIALGAGGLPMGR
                                                                                         1 AIDENKOKALAAALGQIEKQFGKGSIMRLGEDRSMDVKTISTGSLSLDIALGAGGLPMGR
                                                                                                                                                                                                             TGEQALEICDALARSGAVDVIVVDSVAALTPKAEIEGEIGDSHMGLAARMMSQAMRKLAG
                                                                                                                                                                                                                                                                               NLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLDIRRIGAVKEGENVVGS
                                     Gaps
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 DB 8; Length 335;
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100.0%; Score 1678; DB 8;
100.0%; Pred. No. 2.8e-155;
ive 0; Mismatches 0;
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Matches 335; Conservative
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RecA; DNA binding protein; ssDNA binding protein; SSB; DNA strand exchange reaction; site-specific cleavage; mutant; mutein. ADR16428 standard; protein; 335 AA E. coli RecA mutant protein #1. 11-DEC-2003; 2003US-00733782 (first entry) Escherichia coli US2004157248-A1 04-NOV-2004 ADR16428; ADR16428

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The invention relates to an isolated RecA mutant protein, where the protein is either a single mutant RecA protein comprising a deletion of amino acid residues from the carboxyl terminus, or a double mutant RecA protein comprising a deletion of amino acid residues from the carboxyl terminus and an amino acid change from a glutamate to a basic amino acid. The invention also relates to a polymucleotide sequence that encodes the RecA mutant protein, a method of catalysing an in vitro homologous DNA pairing and DNA strand exchange reactions comprising providing an amount of the RecA mutant protein and a method of increasing recombination of the RecA mutant protein and a method of increasing recombination of the RecA mutant protein comprises an enhanced capacity to a cell comprising supplying to the cell an amount of the RecA mutant protein comprises an enhanced capacity to binding protein is the sBDNA binding protein from Escherichia coli (SSB). Creaction as compared to wild-type RecA. The DNA binding protein is the sBDNA binding protein from Escherichia coli (SSB). Creaction as compared to wild-type RecA. The Composition and methods are useful for catalysing homologues DNA pairing and DNA strand exchange creactions in an in vitro or in vivo environment. These may be used in promoting in vitro alterations of genes to permit the rapid construction of dessited gene mutants for industrial and pharmaceutical purposes. The compositic altersations of seal and pharmaceutical purposes. The compositic circuits based on DNA. This sequence represents a RecA mutant protein conting based on DNA. This sequence represents
                                                                                                                                                                                                                                                                                   New RecA mutant proteins comprising a single mutation or a double mutation, useful for catalyzing homologous DNA pairing and DNA strand exchange reactions in an in vitro or in vivo environment.
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                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; SEQ ID NO 1; 34pp; English.
                                                                                                                                                                     Eggler AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutant protein of the invention.
                                                                                                                                                                     Lusetti SL,
                                          COX M M.
LUSETTI S L.
EGGLER A L.
HARUTA N.
                                                                                                                                                                                                                  WPI; 2004-580265/56.
                                                                                                                                                                                                                                           N-PSDB; ADR16429
                                                                                          (EGGL/)
(HARU/)
                                                                                                                                                                     Cox MM,
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. 0 DB 8; Length 335; 99.8%; Score 1674; DB 8. 99.7%; Pred. No. 7e-155; ive 1; Mismatches (Best Local Similarity 99.7 Matches 334; Conservative Query Match

Sequence 335 AA;

1 AIDENKOKALAAALGQIEKQFGKGSIMRLGEDRSMDVKTISTGSLSLDIALGAGGLPMGR

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240 300 181 NLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLDIRRIGAVKEGENVVGS ETRVKVVKNKIAAPFKQAEFQILYGEGINFYGELVDLGVKEKLIEKAGAWYSYKGEKIGQ NLKOSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLDIRRIGAVKEGENVVGS 241 181 241 셤 ò 셤 g ò

301 301

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180 180 240 240 300

IVEIYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSQPD 120

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61 IVELYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSQPD

TGEQALEICDALARSGAVDVIVVDSVAALTPKAEIEGEIGDSHMGLAARMMSQAMRKLAG

121

121 TGEQALEICDALARSGAVDVIVVDSVAALTPKAEIEGEIGDSHMGLAARMMSQAMRKLAG

ETRVKVVKNKIAAPPKQABFQILYGGGINFYGELVDLGVKEKLIEKAGAWYSYKGEKIGQ 300

GKANATAWLKDNPETAKEIEKKVRELLLSNPNSTP 335 301 GKANATAWLKDNPETAKEIEKKVRELLLSNPNSTP 335

ETRVKVVKNKIAAPPKQAEFQILYGEGINFYGELVDLGVKEKLIEKAGAWYSYKGEKIGQ

241 241 301

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181 NLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKPYASVRLDIRRIGAVKEGENVVGS

NLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLDIRRIGAVKEGENVVGS

181

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The invention features to an isolate according to protein is either a single mutant RecA mutant protein, where the protein is either a single mutant RecA mutant protein of amino acid residues from the carboxyl terminus, or a double mutant RecA protein comprising a deletion of amino acid residues from the carboxyl terminus and an amino acid change from a glutamate to a basic amino acid. Terminus and an amend of catalysing an in vitro homologous DNA pairing and DNA strand exchange reactions comprising providing an amount of the RecA mutant protein and a method of increasing recombination of the RecA mutant protein and a method of increasing recombination of the RecA mutant protein and a method of increasing recombination of file RecA mutant protein as comprises an enhanced capacity to a cell comprising supplying to the cell an amount of the RecA mutant protein as comprises an enhanced capacity to displace a DNA binding protein from Escherichia coli (SSB). It also comprises enhanced binding to DNA during a DNA strand exchange reaction as compared to wild-type RecA. The composition and methods are useful for catalysing homologous DNA pairing and DNA strand exchange reactions in an in vitro or in vivo environment. These may be used in creations in an in vitro or in vivo environment. These may be used in creations in an in vitro or in vivo environment. These may be used in creations of desired gene mutants for industrial and pharmaceutical purposes. The mutant proteins may also be used in trargeting the site-specific cleavage of small and large DNAs, or as a based on DNA. This sequence represents the wild-cype RecA protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New RecA mutant proteins comprising a single mutation or a double mutation, useful for catalyzing homologous DNA pairing and DNA strand exchange reactions in an in vitro or in vivo environment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention relates to an isolated RecA mutant protein, where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 352;
                                                                                                                                                                             RecA; DNA binding protein; ssDNA binding protein; SSB;
DNA strand exchange reaction; site-specific cleavage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1674; DB 8;
Pred. No. 7.5e-155;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 5; 34pp; English.
                  ADR16432 standard; protein; 352 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eggler AL,
                                                                                                                                       E. coli wild-type RecA protein.
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                                                                                                                                                                                                                                                                                                                                                               11-DEC-2003; 2003US-00733782.
                                                                                                                                                                                                                                                                                                                                                                                                    12-DEC-2002; 2002US-0432758P.
                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                          COX M M.
LUSETTI S L.
EGGLER A L.
HARUTA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lusetti SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-580265/56.
                                                                                                                                                                                                                                          Escherichia coli.
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                                                          ADR16432;
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ADR16432
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Antisense; prokaryotic essential gene; cell proliferation; drug design.

Escherichia coli.

WO200277183-A2.

03-OCT-2002

21-MAR-2002; 2002WO-US009107.

06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00072851.

2002US-0362699P

06-MAR-2002;

2001US-00815242

21-MAR-2001;

Protein encoded by Prokaryotic essential gene #922.

(first entry)

19-JUN-2003

ABU15395 standard; protein; 353 AA.

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense mucleic acid; (3) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting callular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   screening
                                                                                                                                                                                                                                                                                                                                                                                        Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense nucleic acids, useful for identifying proteins or s
for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                        Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                        Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 25; SEQ ID NO 43319; 1766pp; English.
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Carr GJ,
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Trawick JD,
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Wall D,
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Gaps

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Matches 334; Conservative

Similarity

Best Local

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1 AIDENKQKALAAALGQIEKQFGKGSIMRLGEDRSMDVETISTGSLSLDIALGAGGLPMGR 1 AIDENKQKALAAALGQIEKQFGKGSIMRLGEDRSMDVKTISTGSLSLDIALGAGGLPMGR

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the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profilling a compound a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains, or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids required for dentifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the traget prockaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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99.8%; Score 1674; DB 6; Length 353;
Best Local Similarity 99.7%; Pred. No. 7.6e-155;
Matches 334; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of a wildtype recA protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 353 AA;
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The present sequence represents the recA protein. The wild type recA protein was used to produce hyperrecombinogenic variants (see AAY68928-23), using the method of the invention. The specification describes a method for producing a library of diverse multicellular organisms using pools of male and female gametes. At least one of the male pool or female pools comprises a number of different spacies. The wishe pool or female pools comprises a number of different species. The vishe organisms of a species or of a different species. The vishe organisms or produced from the fertilized gametes are repeatedly crossed to produce a library of diverse organisms, which are selected for a desired trait or property such as heat tolerance, ethanol production or tolerance, acid, improved production and maintenance of enzyme cofactors or NAD(P)H and improved glucose transport. The desired property may be expression of a protein or primary or secondary metabolite. Alternatively the desired companies or compatibility to form a heterokaryon with another
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 TGEQALEICDALARSGAVDVIVVDSVAALTPKAEIEGEIGDSHMGLAARMMSQAMRKLAG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 ETRVKVVKNKIAAPFKQAEFQILYGEGINFYGELVDLGVKEKLIEKAGAWYSYKGEKIGQ 306
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                                                                                                   Zhang Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AIDENKQKALAAALGQIEKQFGKGSIMRLGEDRSMDVKTISTGSLSLDIALGAGGLPMGR
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                                                                                   Minshull J;
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                                                                                                   Krebber CM, Bass S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 358;
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                                                                                     Ness JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1674; DB 3;
Pred. No. 7.7e-155;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             307 GKANATAWLKDNPETAKEIEKKVRELLLSNPNSTP 341
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                                                                                 layre S, Tobin M, Stemmer WPC, Na
PA, Subramanian V, Castle LA, Krv
Huisman G, Yuan L, Affholter JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY68829 standard; protein; 358 AA
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              98US-00116188
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                                                 (MAXY-) MAXYGEN INC.
                                                                                                                                                        WPI; 2000-182446/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                          N-PSDB; AAZ60609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 358 AA;
                                                                                   Del Cardayre S,
              15-JUL-1998;
                                                                                                                                                                                                                                              properties.
                                                                                                       Patten PA,
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AC AAY6
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The present sequence represents a hyperrecombinogenic recA protein. The wild type recA protein (AAY68827) was used to produce hyperrecombinogenic variants using the method of the invention. The specification describes a method for producting a library of diverse multicallular organisms using pools of male and female gametes. At least one of the male pool or female pools of male and female gametes. At least one of the male pool or female pools comprises a number of a different species. The viable organisms to produce from the fertilized gametes are repeatedly crossed to produce a library of diverse organisms, which are selected for a desired trait or property such as heat tolerance, ethanol production or tolerance, acid, improved production and maintenance of enzyme cofactors or NAD(P)H and improved glucose transport. The desired property may be expression of a property is secretion of a protein or primary or secondary metabolite. Alternatively the desired property as secretion of a protein or secondary metabolite, chosen from taxol, cyclosporin A and erythromycin. The desired property may be a comparing to compatibility to form a heterokaryon with another
                                                                                       recA; hyperrecombinogenic variant; male gamete; female gamete;
heat tolerance; ethanol production; ethanol tolerance; metabolite; taxol;
cyclosporin A; erythromycin; meiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Evolution of whole cells and organism by iterative cycles of recombination and selection and screening for acquisition of desired
                                                    Amino acid sequence of a hyperrecombinogenic recA protein clone
                                                                                                                                                                                                                                                                                                                                                                                                                Stemmer WPC, Ne
Castle LA, Kre
Affholter JA;
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                                                                                                                                                                                                                                                                                                   99WO-US015972.
                                                                                                                                                                                                                                                                                                                                      98US-00116188
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                                                                                                                                                                                                                                                                                                                                                                         (MAXY-) MAXYGEN INC.
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                                                                                                                                                                                Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                              Del Cardayre S,
                                                                                                                                                                                                                       WO200004190-A1
                                                                                                                                                                                                                                                                                                                                    15-JUL-1998;
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                 16-MAY-2000
                                                                                                                                                                                                                                                              27-JAN-2000.
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                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Patten PA
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Gaps ö Score 1674; DB 3; Length 358; Pred. No. 7.7e-155; 1; Mismatches 0; Indels (99.8%; Best Local Similarity 99.7 Matches 334; Conservative Similarity Query Match ð 셤

Sequence 358 AA;

ö 120 TGEQALEICDALARSGAVDVIVVDSVAALTPKAEIEGEIGDSHMGLAARMMSQAMRKLAG 180 9 99 61 IVEIYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSQPD AIDENKQKALAAALGQIEKQFGKGSIMRLGEDRSMDVETISTGSLSLDIALGAGGLPMGR 1 AIDENKQKALAAALGQIEKQFGKGSIMRLGEDRSMDVKTISTGSLSLDIALGAGGLPMGR 121 셤 ò ઠે 셤

181 NLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLDIRRIGAVKEGENVVGS 240

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BTRVKVVKNKIAAPFKQAEFQILYGEGINFYGELVDLGVKEKLIEKAGAWYSYKGEKIGQ GKANATAWLKDNPETAKEIEKKVRELLLSNPNSTP 335 307 GKANATAWLKDNPETAKEIEKKVRELLLSNPNSTP 187 247 301 241 ð 셤 ò 셤

ADQ87824 standard; protein; 358 AA

(first entry) 09-SEP-2004 coli recA protein clone #3.

RecA; protoplast formation; gamete; heat tolerance; ethanol production; ethanol tolerance; enzyme cofactor; NAP(P)H; glucose transport; meiosis; heterokaryon; taxol; cyclosportand, erythromycin; viral infection; plant genome shuffling; micropore manipulation; reiterative pooling.

Zhang Y;

<u>ب</u>

Minshull J; , Bass S,

Ness JE, Mi Krebber CM,

Escherichia coli.

AU2004200501-A1.

04-MAR-2004.

09-FEB-2004; 2004AU-00200501.

09-FEB-2004; 2004AU-00200501

(MAXY-) MAXYGEN INC.

Tobin M; Ness JE, Tobin Subramanian V; g g Patten | Krebber (Castle LA, Patte Zhang Y, Krebbe Del Cardayre S; Cox T, Bass S, r JA, Huisman G, J, Stemmer WPC, Minshull J, Yuan L, Co

WPI; 2004-507924/49. N-PSDB; ADQ87817. Evolving cells to acquire a desired property, by forming protoplasts of different cells, fushing protoplasts to form hybrid protoplasts (HP), producing regenerated cells, forming additional HP and producing additional regenerated cells.

Disclosure; Fig 13; 196pp; English.

The invention relates to a method of evolving cells to acquire a desired property by forming protoplasts of different cells, fusing the protoplasts to form hybrid protoplasts, incubating the hybrid protoplasts to produce regenerated cells, repeatedly forming protoplasts from to produce regenerated cells, repeatedly forming protoplasts from cegenerated cells, fusing protoplasts to form hybrid protoplasts in which genomes from protoplasts recombine to form additional hybrid genomes and incubating additional hybrid protoplasts for producing additional cegenerated cells. The invention also relates to a method of producing a library of diverse multicellular organisms involving providing a pool of cegenerated cells. The invention also relates to a method of producing a library of diverse several different gametes derived from the female pool of different species or different species and the male gametes ceferilise the female gametes to grow into reproductively viable cresulting fertilise the female gametes to grow into reproductively viable cresulting fertilise to diverse organisms and selecting the library for a produce a library of diverse organisms and selecting the library for a corganism trapeated properties such as heat tolerance, ethanol production, cethanol tolerance, improved production and maintenance of enzyme cofactors, improved production and maintenance of wall improved

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glucose transport. The desired property is the expression of a protein, primary metabolite or secondary metabolite, the secretion of a protein or secondary metabolite or capacity for meiosis or compatibility to form a heterokaryon with another strain. The secondary metabolite is chosen from taxol, cyclosporin A and erythromycin. The method is also useful for acquisition of desired properties such as enhanced recombinogenicity, gene copy number or gene reductivity and capacity for expression and/or secretion of proteins or secondary metabolites. The method is further useful for predicting efficacy of a drug in treating viral infection, plant genome shuffling, micropore manipulation, producing transgenic animals, improvement of overexpressed genes for a desired phenotype and relevantive pooling and breeding of higher organisms. The cells evolved by the method are useful in molecular genetics. This sequence represents an E. coli recA protein clone used in the method of the invention.
       856666666666665588
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Sequence 358 AA;

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                                                                                AIDENKOKALAAALGQIEKQFGKGSIMRLGEDRSMDVETISTGSLSLDIALGAGGLPMGR
                                                                                                                          61 IVEIYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSQPD
                                                                                                                                                                                    TGEQALEICDALARSGAVDVIVVDSVAALTPKAEIEGEIGDSHMGLAARMMSQAMRKLAG
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                                                                                                                                                                                                                                                                                                               ETRVKVVKNKIAAPFKQAEFQILYGEGINFYGELVDLGVKEKLIEKAGAWYSYKGEKIGQ
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Length 358;
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99.8%; Score 1674; DB 8; 99.7%; Pred. No. 7.7e-155; ive 1; Mismatches 0;
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                                Matches 334; Conservative
                Local Similarity
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ADQ87822 standard; protein; 358 AA coli recA protein clone #1. (first entry) 09-SEP-2004 ADQ87822; RESULT

RecA; protoplast formation, gamete; heat tolerance; ethanol production; ethanol tolerance; enzyme cofactor; NAD(P)H; glucose transport; melosis; heterokaryon; taxol; cyclosporin A; erythromycin; viral infection; plant genome shuffling; micropore manipulation; reiterative pooling.

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Escherichia coli.

04-MAR-2004.

AU2004200501-A1.

09-FEB-2004; 2004AU-00200501.

09-FEB-2004; 2004AU-00200501.

(MAXY-) MAXYGEN INC.

The invention relates to a method of evolving cells to acquire a desired property by forming protoplasts of different cells, fusing the protoplasts to form hybrid protoplasts, incumbating the hybrid protoplasts from to produce regenerated cells, repeatedly forming protoplasts from coproplasts tecombine to form additional hybrid genomes and genomes from protoplasts recombine to form additional hybrid genomes and cincubating additional hybrid protoplasts for producing additional hybrid protoplasts for producing additional protoplasts from male generated cells. The invention also relates to a method of producing a library of diverse multicellular organisms involving providing a pool of alterent gametes one of the male pool or the female pool comprises several different species and the male gometes certilise the female gametes, where one of the male pool or certilise the female gametes or different species and the male gametes or certilise the female gametes or different species and the male gametes or sepation of a species or different species and the male gametes or sepatedly crossing the reproductively viable organisms to produce a library of diverse organisms and selecting the library for a desired trait or property. The methods are useful for evolving cells to crossing train or property in methods are useful for evolving cells to confactors, improved production and maintenance of enzyme coffection, improved production and maintenance of enzyme coffectors, improved production and maintenance of enzyme coffering the nethod secondary metabolite, capacity for metosis or compatibility, to form a certain improved production and maintenance of enzyme corpusing condary metabolite, capacity for metosis or compatibility, or gene reductivity and capacity for expression and or exercition of gene reductivity and capacity for expression and or secondary metabolites. The method is also useful for predicting efficacy of a drug in treating viral infection, the intensity of enganism or secondary metabolite and properties such a sequence represents Evolving cells to acquire a desired property, by forming protoplasts of different cells, fushing protoplasts to form hybrid protoplasts (HP), producing regenerated cells, forming additional HP and producing additional regenerated cells. olecular genetics. This sequence repused in the method of the invention Ness JE, Tobi g B Patten | Krebber (Castle LA, Patto Zhang Y, Krebbo Del Cardayre S; in molecular Disclosure; Fig 13; 196pp; English. Castle an E. coli recA protein clone Yuan L, Cox T, bass c, Affholter JA, Huisman G, Minshull J, Stemmer WPC, are useful WPI; 2004-507924/49. N-PSDB; ADQ87815.

Sequence 358 AA;

120 180 240 99 IVEIYGPESSCKTTLTLQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSQPD TGEQALEICDALARSGAVDVIVVDSVAALTPKAEIEGEIGDSHWGLAARMASQAMRKLAG NLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLDIRRIGAVKEGENVVGS 1 AIDENKOKALAAALGOIEKOFGKGSIMRLGEDRSMDVKTISTGSLSLDIALGAGGLPMGR ; 0 99.8%; Score 1674; DB 8; Length 358; 99.7%; Pred. No. 7.7e-155; Indela 1; Mismatches Best Local Similarity 99.7 Matches 334; Conservative _ 61 67 181 121 Query Match

ETRVKVVKNKIAAPFKQAEFQILYGEGINFYGELVDLGVKEKLIEKAGAWYSYKGEKIGQ 300

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The invention relates to a method of evolving cells to acquire a desired property by forming protoplasts of different cells, fusing the protoplasts to form hybrid protoplasts, incubating the hybrid protoplasts to protoplasts from to produce regenerated cells, repeatedly forming protoplasts from to produce regenerated cells, respectedly forming protoplasts from cegenomes from protoplasts recombine to form additional hybrid genomes and incubating additional hybrid protoplasts for producing additional hybrid protoplasts for producing additional protoplasts recombine to form additional hybrid genomes and incubating additional hybrid protoplasts for producing additional protoplasts several different commerced of the male pool of regenerated cells. The invention also relates to a method of producing a library of diverse wulticellular organisms involving providing a pool of the female gametes to grow into reproductively viable creulting fertilised gametes to grow into reproductively viable creulting fertilised gametes to grow into reproductively viable organisms to grodure a library of diverse organisms and selecting the library for a desired trait or property. The methods are useful for evolving cells to acquire desired properties such as heat tolerance, ethanol production, chance transport. The desired property is the expression of a protein or secondary metabolite or secondary metabolite, capacity for meiosis or compatibility to form a secondary metabolite, rapacity for meiosis or compatibility to form a secondary metabolite is chosen from the exercise or a protein or secondary metabolite is ensembled as a protein or secondary metabolite or secondary metabolite is chosen from the exercise or organisms. The method is also useful for the condition and maintenance or secondary metabolite or secondary metabolite or secondary metabolite or secondary metabolite or secondary metabolite or secondary metabolite or secondary metabolite or secondary metabolite or secondary metabolite or secondary metabolite or secondary metab
247 ETRVKVVKNKIAAPFKQAEFQILYGEGINFYGELVDLGVKEKLIEKAGAWYSYKGEKIGQ 306
                                                                                                                                                                                                                                                                                                                                                                                                  RecA; protoplast formation; gamete; heat tolerance; ethanol production; ethanol tolerance; enzyme cofactor; NAD(PH; glucose transport; meiosis; heterokaryon; taxol; cyclosporin A; erythromycin; viral infection; plant genome shuffling; micropore manipulation; reiterative pooling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Evolving cells to acquire a desired property, by forming protoplasts of different cells, fusing protoplasts to form hybrid protoplasts (HP), producing regenerated cells, forming additional HP and producing
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Subramanian V;
                                                                    Patten PA,
Krebber CM,
                                              GKANATAWLKDNPETAKEIEKKVRELLLSNPNSTP
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Zhang Y, Krebbe
Del Cardayre S;
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                                                                                                                                                                                                           ADQ87821 standard; protein; 358
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Minshull J, Stemmer WPC,
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 coli recA protein.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rech; hyperrecombinogenic variant; male gamete; female gamete;
heat tolerance; ethanol production; ethanol tolerance; metabolite; taxol;
cyclosporin A; erythromycin; meiosis.
            gene copy number or gene reductivity and capacity for expression and/or secretion of proteins or secondary metabolites. The method is further useful for predicting efficacy of a drug in treating viral infection, plant genome shuffling, micropore manipulation, producing transgenic animals, improvement of overexpressed genes for a desired phenotype and reiterative pooling and breeding of higher organisms. The cells evolved by the method are useful in molecular genetics. This sequence represents the E. coli recA protein used in the method of the invention.
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                                                                                                                                                                                                                                     Gaps
acquisition of desired properties such as enhanced recombinogenicity
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                                                                                                                                                                                                     Length 358;
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                                                                                                                                                                                                  Score 1674; DB 8;
Pred. No. 7.7e-155;
1; Mismatches 0;
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/note= "encoded by TCG"
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                                                                                                                                                                                                  Query Match
Best Local Similarity 99.7%;
Matches 334; Conservative
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Escherichia coli.
                                                                                                                                                                    Sequence 358 AA;
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recursive sequence recombination; evolution
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                                                                                                                                                                    The present sequence represents a hyperrecombinogenic recA protein. The wild type recA protein (AAY68827) was used to produce hyperrecombinogenic variants, using the method of the invention. The specification describes as method for producing a library of diverse multicellular organisms using pools comprises a number of different gametes derived from different pools comprises a number of different species. The wiable organisms produced from the fertilized gametes are repeatedly crossed to produce a library of diverse organisms, which are selected for a desired trait or property. The methods can be used to evolve cells to acquire a desired improved production and maintenance, ethanol production or tolerance, acid, improved production and maintenance of enzyme coffactors or NAD(P)H and improved production and maintenance of enzyme coffactors or NAD(P)H and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
                                                                                                                                                                                                                                                                                                                                         improved glucose transport. The desired property may be expression of a protein or primary or secondary metabolite. Alternatively the desired property is secretion of a protein or secondary metabolite, chosen from taxol, cyclosporin A and erythromycin. The desired property may be a capacity for meiosis or compatibility to form a heterokaryon with another
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           Υ,
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                                                                                          Evolution of whole cells and organism by iterative cycles of recombination and selection and screening for acquisition of desired
           Zhang
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           Bass S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
          Castle LA, Krebber CM,
Affholter JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1673; DB 3;
Pred. No. 9.7e-155;
2; Mismatches 0;
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           Subramanian V,
sman G, Yuan L,
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Best Local Similarity 99.4
Matches 333; Conservative
Patten PA, bur. T. Huisman G,
                                                   2000-182446/16
                                                                 N-PSDB; AAZ60613
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 358 AA;
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ID AAW6
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The present invention provides methods employing iterative cycles of recombination and selection/screening for evolution of whole cells and organisms toward acquisition of desired properties, e.g. enhanced recombinosenicity, genome copy number, and capacity for expression and/or secretion of proteins and secondary metabolites. The present sequence represents a wild-type rech procein (designated new Minshall), from an example of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Evolution of whole cells and organisms by recursive DNA sequence recombination in cells to evolve cells having acquired desired function, useful in methods for predicting the efficacy of a drug in treating viral or pathogenic infections.
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                                                                                                                                                                                                                                                                                                                  Minshull J;
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                                                                                                                                                                                                                                                                                                                  Ness JE,
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                                                                                                                                                         98WO-US000852.
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Matches 333; Conservative
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                                                                                                                                                                                                                                                                (MAXY-) MAXYGEN INC
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Escherichia coli
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                                                                                                                                                                                                                                                                                                                     Delcardayre SB,
                                                                                                                                                                                                              17-JAN-1997;
                                                                                                                                                         16-JAN-1998;
                                                                                                       23-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                Patten P;
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120

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240 246 300

(first entry)

Escherichia coli. WO200004190-A1 27-JAN-2000. properties. Synthetic

AIDENKQKALATALGQIEKQFGKGSIMRLGEDRSMDVETISTGSLSLDIALGAGGLPMGR 1 AIDENKQKALAAALGQIEKQFGKGSIMRLGEDRSMDVKTISTGSLSLDIALGAGGLPMGR Gaps ; 0 Score 1669, DB 3; Length 358; Pred. No. 2.4e-154; 2; Mismatches 1; Indels (99.5%; Matches 332; Conservative Local Similarity 7 61 Query Match 셤 셤 ò 8

67

186

127 TGEQALEICDALARSGAVDVIVVDSVAALTPKAEIEGEIGDSHMGLAARMMSQAMRKKLAG

8 셤 ઠ

Amino acid sequence of a hyperrecombinogenic recA protein clone 2.

241

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recA; hyperrecombinogenic variant; male gamete; female gamete; heat tolerance; ethanol production; ethanol tolerance; metabolite; taxol; cyclosporin A; erythromycin; meiosis.

99WO-US015972. 15-JUL-1999; 98US-00116188. 15-JUL-1998;

(MAXY-) MAXYGEN INC.

Stemmer WPC, Ness JE, Minshull J; Castle LA, Krebber CM, Bass S, Zhang Y; Affholter JA; Del Cardayre S, Tobin M, St Patten PA, Subramanian V, (Cox T, Huisman G, Yuan L,

2000-182446/16. N-PSDB; AAZ60610. Evolution of whole cells and organism by iterative cycles of recombination and selection and screening for acquisition of desired

Example 1; Fig 13; 197pp; English.

The present sequence represents a hyperrecombinogenic recA protein. The wild type recA protein (AAY68827) was used to produce hyperrecombinogenic variants, using the method of the invention. The specification describes a method for producing a library of diverse multicellular organisms using pools comprises a number of different gametes derived from different strains of a species or of a different species. The viable organisms produced from the fertilized gametes are repeatedly crossed to produce a library of diverse organisms, which are selected for a desired trait or property. The methods can be used to evolve cells to acquire a desired property. The methods can be used to evolve cells to acquire a desired property such as heat tolerance, ethanol production or tolerance, acid, improved glucose transport. The desired property may be expression of a protein or primary or secondary metabolite. Alternatively the desired property is secretion of a protein or secondary metabolite, chosen from taxol, cyclosporin A and erythromycin. The desired property may be a capacity for meiosis or compatibility to form a heterokaryon with another

Sequence 358 AA;

The invention relates to a method of evolving cells to acquire a desired property by forming protoplasts of different cells fushing the protoplasts of protoplasts incubating the hybrid protoplasts from the protoplasts from the protoplasts from protoplasts recombine to form additional hybrid genomes and concerned cells, fushing protoplasts to form additional hybrid genomes and incubating additional hybrid protoplasts for producing additional hybrid protoplasts for producing additional hybrid protoplasts for producing additional hybrid protoplasts for producing additional hybrid protoplasts for producing additional hybrid protoplasts for producing additional hybrid protoplasts for producing additional hybrid protoplasts for producing additional fregenerated cells. The invention also relates to a method of producing a library of diverse multicellular organisms involving providing a pool of the female gametes and a pool of fleferent strains of a species or different species and the male gametes fertilise the female gametes by permitting at least a portion of the resulting fertilised gametes to grow into reproductively viable organisms to produce a library of diverse organisms and selecting the library for a desired trait or property. The methods are useful for evolving cells to acquire desired properties such as heat tolerance, ethanol production, changing the cofactors, improved production and maintenance of enzyme cofactors, improved production and maintenance of any protein, primary metabolite or secondary metabolite, the secretion of a protein or Disclosure, Fig 13; 196pp; English. IVEIYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSQPD 120 126 121 TGEQALEICDALARSGAVDVIVVDSVAALTPKAEIEGEIGDSHWGLAARMMSQAMRKLAG 180 9 99 IVEIYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSQPD

24.7 ETRVKVVKNKIAAPFKQAEFQVLYGEGINFYGELVDLGVKEKLIEKAGAWYSYKGEKIGG 306 ETRVKVVKNKIAAPFKQAEFQILYGEGINFYGELVDLGVKEKLIEKAGAWYSYKGEKIGQ 300 RecA; protoplast formation; gamete; heat tolerance; ethanol production; ethanol tolerance; enzyme cofactor; NAD(P)H; glucose transport; melosis; heterokaryon; taxol; cyclospornance; erythromycin; viral infection; plant genome shuffling; micropore manipulation; reiterative pooling. by forming protoplasts of Ness JE, Tobin M; Subramanian V; Evolving cells to acquire a desired property, by forming protople different cells, fusing protoplasts to form hybrid protoplasts (the producing regenerated cells, forming additional HP and producing additional regenerated cells. G Pa 301 GKANATAWLKDNPETAKEIEKKVRELLLSNPNSTP 335 Castle LA, Patten Zhang Y, Krebber Del Cardayre S; 307 GKANATAWLKDNPETAKEIEKKVRELLLSNPNSTP AD087823 standard; protein; 358 AA E. coli recA protein clone #2. 09-FEB-2004; 2004AU-00200501. 09-FEB-2004; 2004AU-00200501. (first entry) Yuan L, Cox T, Bass S, Affholter JA, Huisman G, Minshull J, Stemmer WPC, WPI; 2004-507924/49. N-PSDB; ADQ87816. (MAXY-) MAXYGEN INC. Escherichia coli. AU2004200501-A1. 09-SEP-2004 04-MAR-2004. ADQ87823;

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Del Cardayre

Stemmer WPC,

Minshull J,

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Becondary metabolite, capacity for meiosis or compatibility to form a heterokaryon with another strain. The secondary metabolite is chosen from taxol, cyclosporin A and erythrowycin. The method is also useful for acquisition of desired properties such as enhanced recombinosenicity, gene copy number or gene reductivity and capacity for expression and/or secretion of proteins or secondary metabolites. The method is further useful for predicting efficacy of a drug in treating viral infection, plant genome shuffling, micropore manipulation, producing transgenic animals, improvement of overexpressed genes for a desired phenotype and reiterative pooling and breeding of higher organisms. The cells evolved by the method are useful in molecular genetics. This sequence represents an E. coli recA protein clone used in the method of the invention.
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Sequence 358 AA;

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                                                                                                         IVEIYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSQPD
                                                                                                                               67 IVELYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSQPD
                                                                                                                                                           TGEQALEICDALARSGAVDVIVVDSVAALTPKAEIEGEIGDSHMGLAARMMSQAMRKLAG
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                           Gaps
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Length 358;
                         1; Indels
                                                    AIDENKOKALAAALGOIEKOFGKGSIMRLGEDRSMDVKTI
99.5%; Score 1669; DB 8; 99.1%; Pred. No. 2.4e-154; ive 2; Mismatches 1;
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            Best Local Similarity 99.1
Matches 332; Conservative
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ADQ87826 standard; protein; 358 AA (first entry) 09-SEP-2004

E. coli recA protein clone #5.

Rech, protoplast formation, gamete, heat tolerance, ethanol production, ethanol tolerance, enzyme cofactor; NAD(P)H; glucose transport; meiosis; heterokaryon; taxol; cyclosporin A; erythromycin; viral infection; genome shuffling; micropore manipulation; reiterative pooling plant

Escherichia coli.

AU2004200501-A1.

04-MAR-2004.

09-FEB-2004; 2004AU-00200501 09-FEB-2004; 2004AU-00200501

(MAXY-) MAXYGEN INC.

Tobin M; Subramanian V; Ness JE, Patten PA, Krebber CM, Castle LA, Zhang Y, Yuan L, Cox T, Bass S, Affholter JA, Huisman G,

Comparate to form hybrid protoplasts, incubating cells, tusing the protoplasts to form hybrid protoplasts, incubating the hybrid protoplasts or protoplasts to form hybrid protoplasts from to produce regenerated cells, fusing protoplasts to form hybrid protoplasts from to produce regenerated cells, fusing protoplasts to form hybrid protoplasts from protoplasts are ecombine to form additional hybrid genomes and connected cells. The invention also relates to a method of producing a incubating additional hybrid protoplasts for producing additional hybrid protoplasts for producing additional hybrid protoplasts for producing additional hybrid protoplasts for producing additional hybrid protoplasts for producing additional hybrid protoplasts for producing additional hybrid protoplasts for producing a match of producing a library of diverse multicellular organisms, involving providing a pool of the female pool comprises several different gametes derived from a fartilise the female gametes, where one of the male gametes fertilise the female gametes or different species and the male gametes of fertilise the female gametes to grow into reproductively viable organisms to produce a library of diverse organisms and selecting the library for a desired trait or property. The methods are useful for evolving cells to congaried trait or property. The methods are useful for evolving cells to congaried properties such as heat tolerance, ethanol production, cethanol tolerance, improved production and maintenance of enzyme conferced properties such as heat tolerance, ethanol production, conference improved production and maintenance of enzyme conference, improved production and maintenance of enzyme conference, improved production and maintenance of enzyme condary metabolite or secondary metabolite is chosen from the econdary metabolite or secondary metabolite or generation of proteins or secondary metabolite. Capacity for metabolite such and ergulation, producing engale dropperties such as drug in treating viral infection of protein acquire a desired Evolving cells to acquire a desired property, by forming protoplasts of different cells, fusing protoplasts to form hybrid protoplasts (HP), producing regenerated cells, forming additional HP and producing additional regenerated cells. The invention relates to a method of evolving cells to Disclosure; Fig 13; 196pp; English. WPI; 2004-507924/49. N-PSDB; ADQ87819 Sequence 358 AA;

120 67 İVELYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSQPD 126 180 240 246 9 99 187 NLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLDIRRIGAVKEGENVVGS 7 AIDENKOKALAAALGQIEKOFGKGSIMRLGEDRSMDVETISTGSLSLDIALGAGGLPMGR IVEIYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSQPD TGEQALEICDALARSGAVDVIVVDSVAALTPKAEIEGEIGDSHMGLAARMMSQAMRKLAG 181 NLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLDIRRIGAVKEGENVVGS 1 AIDENKQKALAAALGQIEKQFGKGSIMRLGEDRSMDVKTISTGSLSLDIALGAGGLPMGR Gaps ; 0 Length 358; Indels Score 1665; DB 8; Pred. No. 5.9e-154; 2; Mismatches 1; 2; 99.2**%**; 99.1**%**; Best Local Similarity 99.1 Matches 332; Conservative 61 121 Query Match

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ETRVKVVKNKIAAPFKQAEFQILYGEGINFYGELVDLGVKEKLIEKAGAWYSYKGEKIGQ 300

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides methods employing iterative cycles of recombination and selection/screening for evolution of whole cells and organisms toward acquisition of desired properties, e.g. enhanced recombinogenicity, genome copy number, and capacity for expression and/or secretion of proteins and secondary metabolites. The present sequence represents a hyperrecombinogenic variant of a recA protein (see AAW64213), from an example of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli; recA protein; hyperrecombinogenic variant; Minshall; recursive sequence recombination; evolution.
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Pred. No. 7.4e-154;
3; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ness JE,
                                                                                                                                                                                                                                                                                                                                                                                Hyperrecombinogenic variant recA protein clone 4.
   GKANATAWLKDNPETAKEIEKKVRELLLSNPNSTP 335
                                    Stemmer WPC,
                                                                                                                                                                                                    AAW64215 standard; protein; 358 AA
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98.8%;
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Matches 331, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli
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                                                                                                                                                                                                                                                                                                                      28-APR-1999
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301
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                                                                                                                                          RESULT 15
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        Qy
        241 ETRVKVVKNKIAAPPKQAEFQILYGEGINFYGELVDLGVKEKLIEKAGAWYSYKGEKIGG 300

        Db
        247 ETRVKVVKNKIAAPPKQAEFQILYGEGINFYGELVDLGVKEKLIEKAGAWYSYKGEKVGQ 306

        Qy
        301 GKANATAWLKDNPETAKEIEKKVRELLLSNPNSTP 335

        Db
        307 GKANATAWLKDNPETAKEIEKKVRELLLSNPNSTP 341
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Search completed: February 16, 2006, 01:18:52 Job time : 133 secs

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5.1.7
Biocceleration Ltd.
GenCore version (c) 1993 - 2006
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OM protein - protein search, using sw model

Run on:

February 16, 2006, 01:19:09; Search time 25.5 Seconds (without alignments) 1264.024 Million cell updates/sec

US-10-733-782-3 1678 Title: Perfect score: Sequence:

1 AIDENKQKALAAALGQIEKQ.........AKEIEKKVRELLLSNPNSTP 335

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR 80:* 1: pir1:* 2: pir2:* 3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

ıks	Description	recombination prot	_		٠.		c		recombination prot		recombination prot		recombination prot	recombination prot	Reca protein PA361	recombination prot	recombination prot		ㅁ			recombination prot	recombination prot	~	RecA protein NMA16	recA protein [impo	c	recombination prot	recombination prot	
SUMMAKIES	ΩI	ROECA	D91073	H85917	AH0843	AG0401	S31481	S37586	RQEBPM	E82310	S46274	JQ1461	A49929	JC5198	RQPSAA	JN0321	30076	T10482	I39509	JC2406	A47709	A60989	S18728	F81082	F81860	AE3350	RQPSAC	JQ0745	S16896	JC1377
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di	Query Match	99.8	99.8	0.66	97.6	91.2		6.06	89.4	85.3	•	83.9	79.1	78.6	75.6	75.4	•	74.8	٠	•	74.3	73.6	73.1	72.3	•		71.5	71.5	٠	71.3
	Score	1674	1674	1662	1637	1530	1528	1526	1500	1432	1413	1408.5	1328	1319	1268	1265	1263.5	1255	1253	1250			1226.5	1213.5	1212.5		1200.5	199	1199.5	1196.5
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363	416	360	346	348	348	347	343	360	352	343	355	356	374	374	340
71.3	71.3	71.2	70.5	70.4	70.3	6.69	69.7	68.9	68.7	68.5	68.3	68.0	67.9	67.9	67.7
1196.5	1196.5	1194.5	1183.5	1181	1179.5	1173	1170	1156	1153	1149.5	1146.5	1141	1139	1139	1136
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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SGLT	EC P

RESULT 1

ROBCA
recombination protein recA [validated] - Escherichia coli (strain K-12)
N;Alternate names: recombinase A
C;Species: Escherichia coli
C;Species: Bacherichia coli
C;Species: 1-Uul-1800 #sequence revision 14-Nov-1997 #text change 09-Jul-2004
C;Accession: G65049; A93847; A93846; S11931; S63525; S69129; S63979; A03548
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C, Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503

A; Accession: G65049
A; Status: nucleic acid sequence not shown; translation not shown
A; Accession: G65049
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-353 cBLAT>
A; Cross-references: UNIPROT: P03017; UNIPARC: UP10000112C1C; GB: AE000354; GB: U00096; NID
A; Experimental source: strain K:12, substrain MG1655
A; Cross-references: UNIPROT: P0304, H.; Ogawa, T.

A; Molecule type: DNA A; Residues: 2-353 <SAN>

A;Cross-references: UNIPARC:UP10000112C17; GB:V00328; GB:J01672; NID:g42672; PIDN:CAA23 R;Zhao, X.J.; McEntee, K.
Mol. Gen. Genet. 222, 369-376, 1990
A;Title: DNA sequence analysis of the recA genes from Proteus vulgaris, Erwinia carotov A;Reference number: S11931; MUID:91109725; PMID:2274037
A;Accession: S11931
A;Molecule type: DNA

A;Residues: 2.353 <ZHA>
A;Cross-references: UNIPARC:UPI0000112C17; GB:X55552; NID:942678
A;Note: this ORF is not annotated in GenBank entry ECRECAGEN, release 109.0
R;Morimatsu, K.; Horii, T.

Eur. J. Blochem. 234, 695-705, 1995 A,Title: DNA-binding surface of RecA protein. Photochemical cross-linking of the first A,Reference number: 863525; MUID:96096752; PMID:8529655

A; Accession: S63525

A;Status: preliminary A;Molecule type: protein A;Residues: 65-69;90-97;179-184;200-207;258-265;304-311;323-331 <MOR1> A;Cross-references: UNIPARC:UPI00001748A7; UNIPARC:UPI00001748A8; UNIPARC:UPI00001748A5

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99.8%;
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Matches 334; Conservative
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R;Morimateu, K.; Horli, T.

Bur. J. Blochem. 228, 772-778, 1995

A;Title: The DNA-binding site of the RecA protein. Photochemical cross-linking of Tyrlo3

A;Reference number: 569129; MUID:95255284; PMID:773176

A;Reference number: 569129; MUID:95255284; PMID:773176

A;Reference number: 569129

A;Residues: Porcein

A;Residues: WINFARC:UF100001748AB

R;Gardmer, R. V.; Voloshin, O.N.; Camerini-Otero, R.D.

Bur. J. Biochem. 233, 419-425, 1995

A;Residues: WINFARC:UF100001748AF

Bur. J. Biochem. 233, 419-425, 1995

A;Residues: XX. 187-199, 122-194 cGAR>
A;Residues: XX. 187-199, 122-194 cGAR>
A;Residues: XX. 187-199, 122-194 cGAR>
A;Residues: XX. 187-199, 122-194 cGAR>
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A;Residues: XX. 187-199, 122-194 cGAR>
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A;Residues: XX. 187-199, 122-194 cGAR>
A;Residues: XX. 187-199, 122-194 cGAR>
A;Residues: XX. 187-199, 122-194 cGAR>
A;Contents: annotation; Aray crystallography, 2.; Yokoyama, S.; Shibata, T.

B;Athara, H.; Ito, Y.; Kurumizaka, H.; Teada, T.; Yokoyama, S.; Shibata, T.

B;Athara, H.; Ito, Y.; Kurumizaka, H.; Teada, T.; Yokoyama, S.; Shibata, T.

A;Genetics: annotation; conformation by (1)H- and (15)R-NMR, residues 269-331

C;Genetics: annotation; conformation by (1)H- and (15)R-NMR, residues 269-331

C;Genetics: A;Gene: recA

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D91073
RecA protein [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
C;Species: Escherichia coli
C;Species: Bacherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: D91073
R;Hayasahi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
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99.8%; Score 1674; DB 1;
Best Local Similarity 99.7%; Pred. No. 3.6e-106;
Matches 334; Conservative 1; Mismatches 0;
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DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: D91073
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-353 cHAX>
A;Cross-references: UNIPROT:P03017; UNIPARC:UPI0000112C1C; GB:BA000007; PIDN:BAB36979.1;
A;Experimental source: strain O157:H7, substrain RIMD 0509952
A;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: recombination protein recA
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A,Experimental source: strain O157:H7, substrain BDL933
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Pred. No. 3.6e-106;
1; Mismatches 0;
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C,Superfamily: recombination protein recA
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A; Residues: L-353 APAR>
A; Residues: L-353 APAR>
A; Cross-references: UNIPARC:UPI000005A334; GB:AL513382; PIDN:CAD05935.1; PID:gl6503906;
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C,Superfamily: recombination protein recA
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62
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RecA protein [imported] - Yersinia pestis (strain C092)
(;Species: Yersinia pestis
C;Species: Versinia pestis
C;Species: Versinia pestis
C;Accession: AG0401
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.F. (Abarkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.F. (Abarteraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davies, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, A.Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MuID:21470413; PMID:11586360
A;Accession: AG0401
A;Accession: AG0401
A;Accession: Ag0401
A;Residues: 1-356 <KURPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:P37858; UNIPARC:UPI0000165AF8; GB:AL590842; PIDN:CAC92539.1
C;Genetics:
A;Gene: reca
C;Superfamily: recombination protein reca
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NyAlternate names: recombinase A
NyAlternate names: recombinase A
Syspecies Enterobacter agglomerans
C;Bete: 13-0an-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S31481
R;Rappold, C.S.J.; Klingmueller, W.
submitted to the EMBL Data Library, January 1993
A;Description: Cloning and sequencing of the recA gene from Enterobacter agglomerans 33
A;Reference number: S31480
A;Reference number: S31481
A;Reference preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-354 < RAP>
A;Cross-references: UNIPROT: P33037; UNIPARC: UPI000016EC3A; GB:L03291; EMBL: Z19517; NID:
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91.2%; Score 1530; DB 2; Length 3
Best Local Similarity 91.6%; Pred. No. 2.1e-96;
Matches 304; Conservative 15; Mismatches 13; Indels
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C;Superfamily: recombination protein recA
C;Keywords: ATP; DNA binding; DNA recombination; DNA
C;Keywords: ATP; DNA binding; DNA recombination; DNA
F;67-74/Region: nucleotide-binding motif A (P-loop)
F;141-146/Region: nucleotide-binding motif B
F;73/Binding site: ATP (Lys) #status predicted
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CjAccession: E82310
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Description: plays an essential role in homologous recombination, in induction of the C; Superfamily: recombination protein recA (S. Superfamily: recombination protein recA (S. Superfamily: recombination; DNA recombination; DNA repair; nucleotide binding; P-loop; F; 67-74/Region: nucleotide-binding motif A (P-loop) F; 141-146/Region: nucleotide-binding motif B F; 73/Binding site: ATP (Lys) #status predicted
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61 IVEIYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSQPD 120
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                                                                                                                                                                recombination protein recA - Proteus mirabilis
N;Alternate names: recombinase A
C;Species: Proteus mirabilis
C;Species: Proteus mirabilis
C;Accession: S04606
R;Akaboshi, E.; Yip, M.L.R; Howard-Flanders, P.
Nucleic Acids Res. 17, 4390, 1389
A;Title: Nucleotide sequence of the recA gene of Proteus mirabilis.
A;Reference number: S04606; MUID:89295502; PMID:2544862
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89.1%; Pred. No. 2.2e-94;
tive 22; Mismatches 14;
                                                    GKANATAWLKDNPETAKEIEKKVRELLLSNPN 332
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GKANASNYLKENPANABLDKKLREMLLNGGN
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Best Local Similarity 89.1%;
Matches 294; Conservative
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A; Residues: 1-355 <AKA>
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C; Function:
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                                                    AIDENKOKALAAALGQIEKQFGKGSIMRLGEDRSMDVKTISTGSLSLDIALGAGGLPMGR
                                                                                 AIDENKQKALAAALGQIEKQFGKGSIMRLGEDRSMDVETISTGSLSLDIALGAGGLPMGR
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                   Indels
   .8%; Pred. No. 2.8e-96; s 16; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                            302 GKANSCNYLKENPKVAAELDKKLRDMLLS 330
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Matches 304; Conservative
                 302; Conservative
 Similarity
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A; Molecule type: DNA
A; Residues: 1-348 <TOL>
A; Residues: 1-348 <TOL>
A; Residues: 1-348 <TOL>
A; Residues: 1-348 <TOL>
A; Residues: 1-348 <TOL>
A; Residues: 1-348 <TOL>
A; Experimental source: strains 775 and 531A
A; Experimental source: strains 775 and 531A
A; Genetics:
A; Genetics:
A; Genetics: recA
C; Function:
A; Description: plays an essential role in homologous recombination, in induction of the C; Superfamily: recombination protein recA
C; Superfamily: recombination protein recA
C; Keywords: ATP; DNA binding; DNA recombination, DNA repair; nucleotide binding; P-loop F; 55-72/Region: nucleotide-binding motif B
F; 55-72/Region: nucleotide-binding motif B
F; 55-73/Region: ATP binding #status predicted
F; 71/Binding site: ATP (Lys) #status predicted
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N;Alternate names: recombinase A
C;Species: Vibrio anguillarum
C;Species: Vibrio anguillarum
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: JQ1461
R;Tolmasky, M.E.; Gammie, A.E.; Crosa, J.H.
Gene 110, 41-48, 1992
A;Fitle: Characterization of the recA gene of Vibrio anguillarum.
A;Reference number: JQ1461; MUID:92184113; PMID:1544576
                                                                                                                                                                                                                                                                          241 TRIKVVKNKIAAPFKEANTQIMYGQGFNREGELIDLGVKHKMVEKSGAWYSYNGDKIGQG
                         61 VEILGPESSGKTTLTLELIAAAQREGKTCAFIDTEHALDPVYAKKLGVNIDBLLVSQPDT
                                                                                                                                                                                           1 MDENKOKALAAALGOIEKOFGKGSIMRLGDNRTMDVETISTGSLSLDIALGAGGLPMGRI
    VEIYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSOPDT
                                                                                   GEQALEICDALARSGAVDVIVVDSVAALTPKAEIEGEIGDSHMGLAARMMSQAMRKLAGN
                                                                                                         LKQSNTLLIPINQIRMKIGVMFGNPETTTGGNALKPYASVRLDIRRIGAVKEGENVVGSE
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                                                                                                                                                                                                                                                                                                                                  KANATAWLKDNPETAKEIEKKVRELLLSNPN 332
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                                                     A Molecule Type: DNA

A Residues: 1-412 <HEI>

A) Crossiuces: 1-412 <HEI>

A) Crossiuces: 1-412 <HEI>

A) Experimental source: serogroup 01, strain N16961, blotype Bl Tor

C) Genetics:

A) Gene: VOG533

A) Map position: 1

C) Superfamily: recombination protein recA
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C; Superfamily: recombination protein recA
C; Keywords: ATP: DNA binding; DNA recombination; DNA repair; nucleotide binding; P-loop;
P;153-144 (Region: nucleotide-binding motif A (P-loop)
P;139-144 (Region: nucleotide-binding motif B
P;71/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cyacte: 27-Jan. 1955 #sequence_revision 27-Jan. 1959 #text_change 02-Feb-2001
Cyactesation: 846274
Ry Strocher, U.H.; Lech, A.J.; Manning, P.A.
Ry Strocher, U.H.; Lech, A.J.; Manning, P.A.
Ry Strocher, U.H.; Lech, A.J.; Manning, P.A.
Ry Strocher, U.H.; Lech, A.J.; Manning, P.A.
A.P. Gene Gener. 244, 255-302, 1994
A.P. Stelerence number: 846274; MUID: 94335880; PMID: 8058040
A.P. Status: proliminary
A.M. Status: proliminary
A.M. Residus: 1-354 <STR>
A. Strocher Strocher Company
A. Cross-references: UNIPARC: UPI0000170586; EMBL: X71969; NID: 9530269; PIDN: CAA50764.1; E.C. Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRVKVVKNKIAAPFKQAEFQILYGEGINFYGELVDLGVKEKLIEKAGAWYSYKGEKIGQG 301
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N;Alternate names: recombinase A
C;Species: Vibrio cholerae
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                     239 LKQSNCMCIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLDIRRTGAIKEGEEVVGNE
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A; Reference number: A82035; MUID: 20406833; PMID: 10952301
                                                                                                                                                                                                                                            85.3%; Score 1432; DB 2;
84.0%; Pred. No. 1.1e-89;
iive 32; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.2%; Score 1413; DB 2;
82.8%; Pred. No. 1.7e-88;
ive 32; Mismatches 25;
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Matches 278; Conservative
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                                      Status: preliminary
                   Accession: E82310
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Best Local Simi
Matches 274;
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                                                                                                                                                                  27-Feb-1997 #text_change 09-Jul-2004
                                                                                                                                                                               C,Accession: JC5198
R;Umelo, E.; Noonan, B.; Trust, T.J.
Gene 175, 133-136, 1996
A,Title: Cloning, characterization and expression of the recA gene A,Title: Cloning, Characterization and expression of the recA gene A,Facession: JC5198; MUID:97074662; PMID:8917089
A,Facession: JC5198
A,Status: preliminary
A,Rolecule type: DNA
A,Residues: 1-353 <UME>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302 KANATAWLKDNPETAKEIEKKVRELLLS 329
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                                                                                 N;Alternate names: recombinase A
C;Species: Aeromonas salmonicida
C;Date: 27-Feb-1997 #sequence_revision
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A49293

recombination protein rech - Haemophilus influenzae (atrain Rd KW20)

NiAlternate names: rect 1 protein; recombinase A
C; Species: Haemophilus influenzae
C; Species: Haemophilus influenzae
C; Species: Haemophilus influenzae
C; Species: Haemophilus influenzae
C; Species: Haemophilus influenzae
C; Species: Haemophilus influenzae
C; Species: Haemophilus influenzae
C; Species: Haemophilus influenzae
C; Species: Haemophilus influenzae
C; A102034
C; A202034
A; A102034
A; A102034
A; Reference number: A49329; MUID: 94042901; PMID: 8226674
A; Residues: 1-354 - ZML
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301 KANACKFLRENPAAMALDTKLREMLL-NP
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A;Residues: 1.346 <SAN1>
A;Cross-references: UNIPROT: P08280; UNIPARC: UPI0000133516; GB: X05691; NID: g45413; PIDN: C
A;Cross-references: UNIPROT: P08280; UNIPARC: UPI0000133516; GB: X05691; NID: g45413; PIDN: C
A;Note: part of this sequence, including the amino end of the mature protein, was confin R;Zaitsev, E.N.; Krjukov, V.M.; Kuzmin, N.P.; Alekseev, A.A.; Lanzov, V.A.
Submitted to the EMBL Data Library, March 1990
A;Description: Restriction polymorphism and nucleotide sequence substitutions in the rec
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Nighternate names: recombinase A Cipportes Pseudomonas aeruginosa Cipportes: Pseudomonas aeruginosa Cipportes: 30-Sep-1990 #sequence revision 30-Sep-1990 #text_change 09-Jul-2004 Cipacession: S06265; S10458; A49854; JN0304; G83192
R;Sano, Y.; Kageyama, M. R;Sano, Y.; Kageyama, M. Mol. Genet. 208, 412-419, 1987
N;Title: The sequence and function of the recA gene and its protein in Pseuc A;Reference number: S06265; MUID:88038334; PMID:2823059
                                                                                                                                                                                                                                                                                                                  122 GEQALEICDALARSGAVDVIVVDSVAALTPKAEIEGEIGDSHMGLAARMMSQAMRKLAGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 LKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLDIRRIGAVKEGENVVGSE
                                                                                                                                          2 IDBNKQKALAAALGQIEKQFGKGSIMRLGEDRSMDVKTISTGSLSLDIALGAGGLPMGRI
                                                                          Gaps
                                                                          ö
          Length 353;
                                                                          Indels
1 Similarity 79.0%; Score 1319; DB 2; Similarity 79.0%; Pred. No. 4e-82; S9; Conservative 31; Mismatches 38;
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RESULT 13

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UNABLE TO THE COMPINATION PROTEIN RECA - Azotobacter vinelandii

N.Alternate names: recombinase A

C.Species Azotobacter vinelandii

C.Species Azotobacter vinelandii

C.Species Azotobacter vinelandii

C.Species Azotobacter vinelandii

C.Species Azotobacter vinelandii

C.Species Azotobacter vinelandii

R.Kenkatesh, T.V.; Das, H.K.

G.Accession: JN0321

R.Kenkatesh, T.V.; Das, H.K.

R.Kenkatesh, T.V.; Das, H.K.

R.Kenkatesh, T.V.; Das, H.K.

R.Kenkatesh, T.V.; Das, H.K.

R.Kenkatesh, T.V.; Das, H.K.

R.Kenkatesh, T.V.; Das, H.K.

A.Reference number: JN0321; MUID:9225347; PMID:1563632

A.Title: The Azotobacter vinelandii recA gene: sequence analysis and regulation of expx

A.Residues: 1-349 ckEN>

A.Residues: 1-349 ckEN>

A.Residues: 1-349 ckEN>

A.Residues: 1-349 ckEN>

A.Residues: 1-349 ckEN>

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A.Residues: 130 ckEN>

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A.Residues: 150 ckEN>

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         completed: February 16, 2006, 01:24:57
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A; Cresterious: 1-346 < 2415
A; Cresterious: 1-346 < 2415
A; Cresterious: 1-346 < 2415
B; Sano, Y.
B; Sano, Y.
D; Bacteriol. 175, 2451-4154, 1993
A; Title: Role of the recA-related gene adjacent to the recA gene in Pseudomonas aeruginc
A; Reference number: A49854; MUID:93224470; PMID:8468303
A; Accession: A49854
A; Cresterious: Preliminary
A; Rocession: A49854
A; Cresterious: Preliminary
A; Rocession: A49854
A; Cresterious: DNA
A; Residues: 313-346 < SAN2>
A; Crosterious: DNA
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A. Residues: 1-332, 'L', 334-346 «KRY»

A. Residues: 1-332, 'L', 334-346 «KRY»

A. Crose=references: UNIPARC:UP100001748B2; GB:X52261; NID:g45383; PIDN:CAA36504.1; PID:g

A. Experimental source: strain PAM 7

A. Note: the authors translated the codon CTG for residue 333 as Val

R. Stover. C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

J. Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A. Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A; Reference number: A62950; MUID:20437337; PMID:10984043
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Experimental source: strain PAO1
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C; Superfamily: recombination protein recA
C; Superfamily: recombination protein recA
C; Seywords: ATP: DNA binding; DNA recombination; DNA repair; nucleotide binding; P-loop; F; 65-72/Region: nucleotide-binding motif A (P-loop)
F; 139-144/Region: nucleotide-binding motif B
F; 71/Binding site: ATP (Lys) #status predicted
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; Pred. No. 1.1e-78;
42; Mismatches 42; Indels
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Best Local Similarity 74.4%
Matches 244; Conservative
A;Reference number: S10458
A;Accession: S10458
                                                                                         A; Molecule type: DNA
A; Residues: 1-346 <ZAI>
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Molecule type: DNA
Residues: 1-346 <STO>
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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EMBL; BA000007; BAB36979.1; -; Genomic_DNA.
PIR; D91073; D91073.
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MBDLINE=21156231; PubMed=11258796;
Hayashi T. Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Complete genome sequence of enterohemorrhagic Escherichia coli
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-!- FUNCTION: Can catalyze the hydrolysis of ATP in the presence of single-stranded DNA, the ATP-dependent uptake of single-stranded DNA by duplex DNA, and the ATP-dependent hybridization of homologous single-stranded DNAs. It interacts with lexA causing its activation and leading to its autocatalytic cleavage (By
        vibrio
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
13-SRP-2005 (Rel. 48, Last annotation update)
RecA protein (Recombinase A).
Name=recA, OrderedLocusNames=z4002, EC83556;
Escherichia coli O157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriais Escherichia.
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SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the recA family.
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RECA_PASMU
RECA_PASIN
Q40MV2_LABEN
RECA_PSEOL
Q50UB8_IDILO
RECA_AERSA
RECA_MANSM
RECA_MIGBR
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STRAIN=O6:H1 / CFT073 / ATCC 700928 / UPEC;
MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.25529799;
WEICH R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli.";
proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
-!-FUNCTION: Can catalyze the hydrolysis of ATP in the presence of single-stranded DNA, the ATP-dependent uptake of single-stranded
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Name=recA; OrderedLocusNames=c3253;

Recherichia coli 06.

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

Enterobacteriaceae; Escherichia.
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R HAMAP; MF_00268; -; 1.

R InterPro; IPR001553; RecA.

R Pfam; PF00154; RecA; 1.

R PRINTS; PR00142; RECA.

R PTODOM; PD000229; RecA; 1.

R PROSITE; PS00121; RECA_1 1.

R PROSITE; PS00121; RECA_2 1.

R PROSITE; PS00121; RECA_2 1.

R PROSITE; PS00163; RECA_2 1.

R PROSITE; PS00163; RECA_2 1.

R PROSITE; PS00163; RECA_2 1.

R PROSITE; PS00163; RECA_3 1.

R PROSITE; PS00163; RECA_3 1.

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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DNA by duplex DNA, and the ATP-dependent hybridization of homologous single-stranded DNAs. It interacts with lexA causing its activation and leading to its autocatalytic cleavage (By
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Enterobacteriaceae; Escherichia.
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Name=recA; Synonyms=lexB, recH, rnmB, tif, umuB, zab; OrderedLocusNames=b2699;
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99.7%; Pred. No. 1.6e-103;
tive 1; Mismatches 0;
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21-UUL-1986 (Rel. 01, Created)
12-UUL-1986 (Rel. 01, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
                                                                                                                                                                                          SUBCELLULAR LOCATION: Cytoplasmic (By si SIMILARITY: Belongs to the recA family.
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InterPro; IPR003593; AAA ATPase.
InterPro; IPR001553; RecA.
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analyzis of its sequence features.";
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MEDINE-95255284; PubMed=7737176;
MOXIMARESU K., Horii T.;
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MEDLINE=96067680; PubMed=7588783;
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Erwinia carotovora, Shigella flexneri and Escherichia coli B/r.";
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"The RecA hexamer is a structural homologue of ring helicases.";
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                                      MEDLINE=80145618; PubMed=6244554;
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Proc. Natl. Acad. Sci. U.S.A. 77:313-317(1980).
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STRAIN=K12 / MG1655;
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MEDLINE=97185905; PubMed=9033586;
Yu X., Egelman E.H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli RecA protein.";
Eur. J. Biochem. 233:419-425(1995).
                                                                                                                                                                [3]
NUCLEOTIDE SEQUENCE.
MEDLINE=91109725; PubMed=2274037;
                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=K12;
MEDLINE=97349980; PubMed=9205837;
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                                                                                                                                                                                                                                                                              MG1655;
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 NCBI_TaxID=562;
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Park Y.C., Shin H.J., Kim Y.C.;
"Cloning and nucleotide sequence of the recA gene from Shigella sonnei
"Cloning and nucleotide sequence of the recA gene from Shigella sonnei
"Cloning and nucleotide sequence of the EMBL/GenBank/DDBJ databases.
"Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: Can catalyze the hydrolysis of ATP in the presence of
single-stranded DNA, the ATP-dependent uptake of single-stranded
DNA by duplex DNA, and the ATP-dependent hybridization of
homologous single-stranded DNAs. It interacts with lexA causing
its activation and leading to its autocatalytic cleavage.
-! SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-! SIMILARITY: Belongs to the recA family.
                                                                                                                                                                                                                                                                                                                                                           BIRVKVVKNKIAAPPKQABPQILYGEGINFYGELVDLGVKEKLIBKAGAMYSYKGEKIGQ
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Enterobacteriaceae, Shigella.
NCBI_TaxID=624;
                                                                                                                                   ö
                   recombination;
                                                                                                        Length 352;
PROSITE; PS50163; RECA 3; 1.

ATP-binding; Complete proteome; DNA damage; DNA recombinat DNA repair; DNA-binding; Nucleotide-binding; SOS response. INIT MET 0 0 By similarity.

NP BIND 66 73 ATP (By similarity).

SEQUENCE 352 AA; 37842 MW; 989802378EC4A402 CRC64;
                                                                                                                                   Indels
                                                                                                      Score 1674; DB 1;
Pred. No. 1.6e-103;
1; Mismatches 0;
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30-MAY-2000 (Rel. 39, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
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HASP; P03017; ZREB.
SWR; Q9ZPF6; 3-328.
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                                                                                                     Query Match

Best Local Similarity 99.7%;
Matches 334; Conservative
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                                                                                                                                                                                                                                       SMART; SM00382; AAA; 1.
TIGRFAMS; TIGR02012; tigrfam_recA; 1.
PROSITE; PS00321; RECA_1; 1.
PROSITE; PS50162; RECA_2; 1.
AFP-binding; DNA damage; DNA recombination; DNA repair; DNA-binding; Nucleotide-binding; SOS response.
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"Complete genome sequence of a multiple drug resistant Salmonella enterica servoar Typhi CT18.";
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Salmonella typhi.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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352 AA; 37799 MW; EEC50231893AA40C CRC64;
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Pred. No. 4.6e-103;
1; Mismatches 1;
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HAWAP; MF_00268; -; 1.
InterPro; IPR001559; AAA ATPase.
InterPro; IPR001553; RecĀ.
Pfam; PF00154; RecA; 1.
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ProDom; PD000229; RecA; 1.
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                                                                                                                                                                                                                                                                                                          J. Bacteriol. 185:2330-2337 (2003).
-I- FUNCTION: Can catalyze the hydrolysis of ATP in the presence of single-stranded DNA, the ATP-dependent uptake of single-stranded DNA by duplex DNA, and the ATP-dependent hybridization of homologous single-stranded DNAs. It interacts with lexA causing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                       STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
DOI=10.1128/JB.185.7.2330-2337.2003;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          its activation and leading to its autocatalytic cleavage (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repair; DNA-binding; Nucleotide-binding; SOS response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 73 ATP (By similarity).
352 AA; 37813 MW; F24E51CB9A31B818 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1637; DB 1;
Pred. No. 4.6e-101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL627276; CAD05935.1; -; Genomic_DNA
EMBL; AE016843; AAO70291.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00142; RECA.
Prodom, PD000229; RECA; 1.
SMART; SM00382; AAA; 1.
TIGRFAMB; TIGR02012; tigrfam_recA; 1.
PROSITE; PS00321; RECA_1; 1.
PROSITE; PS50162; RECA_2; 1.
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SMR; P65978; 3-328.
HAMAP; MF 00268; -; 1.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR001553; RecĀ.
Pfam; PF00154; RecA; 1.
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Nature 413:848-852(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Can catalyze the hydrolysis of ATP in the presence of single-stranded DNA, the ATP-dependent uptake of single-stranded DNA by duplex DNA, and the ATP-dependent hybridization of homologous single-stranded DNAs. It interacts with lexA causing its activation and leading to its autocatalytic cleavage (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.
NCBI_TaxID=602;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1] "NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=LTZ / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the recA family.
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4.6e-101;
301 GKANATTWLKENPATAKEIEKRVRELLLSNQNATP 335
                                                                                                                                                                                   P65977; QRXETO;
28-FEB-2003 (Rel. 41, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
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6; Mismatches
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HSSP; P03017; 2REB.
SMR; P65977; 3-328.
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InterPro; IPR001553; RecA.
InterPro; IPR001553; RecA.
PRINTS; PR00142; RECA.
ProDom; PD000229; RECA.
ProDom; P000182; AAA; 1.
SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                                RecA protein (Recombinase A).
Name=recA; OrderedLocusNames=STM2829;
Salmonella typhimurium.
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PROSITE, PS50162; RECA-2; 1.
PROSITE, PS50163; RECA-3; 1.
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Matches 325; Conservative
                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           StyGene; SG????; recA.
HAMAP; MF_00268; -; 1.
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Best Local Similarity
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241
     62 IVBIYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPVYARKLGVDIDNLLCSQPD 121
                                                                                                                                                                                                                                                                         ETRVKVVKNKIAAPFKQAEFQILYGEGINFYGELVDLGVKEKLIEKAGAWYSYKGEKIGQ 300
                                                                                                                                                                                                                                                                                                    BIRVKVVKNKIAAPFKQAEFQILYGEGINFYGELVDLGVKEKLIEKAGAWYSYNGEKIGQ 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VICTORIDE SEQUENCE.

STRAIN-ATCC 9150 / SARB42;

WUNDEGG-1551808;

WUNDEGG-15518082;

WENDEGG-15518082;

WACTO-11 and M., Sanderson K.E., Clifton S.W., Latreille P.,

McClelland M., Sanderson K.E., Clifton S.W., Latreille P.,

McClelland M., Sanderson K.E., Clifton S.W., Latreille P.,

McClelland M., Sanderson K.E., Clifton S.W., Latreille P.,

Markins C.R., Wang C., Wayen C., Berghoff A., Elliott G.,

Kohlberg S., Strong C., Du F., Carter J., Kremizki C., Layman D.,

Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P.,

Malson R.K.;

Comparison of genome degradation in Paratyphi A and Typhi, human-

restricted servovars of Salmonella enterica that cause typhoid.";

Nat. Genet. 36:1268-1274 (2004).

MR. Genet. 36:1268-1274 (2004).

MR. SRR; OSPELS; 4-229.
                                                                                                                                                                                                       NIKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLDIRRIGAVKEGDNVVGS
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Enterobacteriaceae, Salmonella.
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GO; GO:0005684; F:ATP binding; IEA.
GO; GO:0008094; F:DNA-dependent ArPase activity; IEA.
GO; GO:0011111; F:Nucleoside-triphosphatase activity; IEA.
GO; GO:0011111; F:nucleoside-triphosphatase activity; IEA.
GO; GO:000116; F:nucleoside-triphosphatase activity; IEA.
GO; GO:000510; F:DNA recombination; IEA.
GO; GO:0005391; P:DNA repair; IEA.
InterPro; IPR001553; RecĀ.
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
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Name=recA; OrderedLocusNames=SPA2687;
Salmonella paratyphi-a.
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TIGREAMS; TIGRO2012; tigrfam_recA; 1.
PROSITE; PS00321; RECA_1; 1.
PROSITE; PS50162; RECA_2; 1.
PROSITE; PS50163; RECA_2; 1.
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ProDom; PD000229; RecA; 1.
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QSPF15;
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Matches 324; Conservative
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SEQUENCE 353 AA;
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ETRVKVVKNKIAAPFKQAEFQILYGEGINFYGELVDLGVKEKLIEKAGAWYSYKGEKIGQ 300
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                                                                                                  181 NIKOSNTLIFINOIRMKIGVMFGNPETTTGGNALKFYASVRLDIRRIGAVKEGENVVGS
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                                                                         TGEQALEICDALARSGAVDVIVVDSVAALTPKAEIEGEIGDSHMGLAARMMSQAMRKLAG
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Pubmed=15781495; DOI=10.1093/nar/gki297;
Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,
Wang H.-S., Lee Y.-S.,
Ine Y.-S., Lee Y.-S.,
highly invasive and resistant zononcic pathogen.";
Nucleic Acids Res. 33.1690-1698(2005).
EMBL; AE017220; AAX66668.1; -; Genomic_DNA.
SNR; OSTKU4; 4-329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DNA strand exchange and recombination protein with proteiase and
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GO; GO:0005544; F:ATP binding; IEA.
GO; GO:0008094; F:DNA-dependent ArPase activity; IEA.
GO; GO:000104; F:DNA-dependent ArPase activity; IEA.
GO; GO:0017111; F:nucleoside-triphosphatase activity; IEA.
GO; GO:000116; F:nucleotide binding; IEA.
GO; GO:0006281; P:DNA recombination; IEA.
GO; GO:0006281; P:DNA repair; IEA.
InterPro; IRR001553; RecĀ.
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PRINTS; PR00142; RECA.
SMART; SM00382; AAA; 1.
TIGRFAMA; TIGR02012; tigrfam_recA; 1.
PROSITE; PS00321; RECA 1; 1.
PROSITE; PS50162; RECA-2; 1.
PROSITE; PS50163; RECA-2; 1.
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Q57KU4;
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Matches 325; Conservative
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SEQUENCE 353 AA
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TIGRFAMS; TIGR02012;
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                                                                                                                                                                            TGEQALEICDALARSGAVDVIVVDSVAALTPKAEIEGEIGDSHMGLAARWASQAMRKLAG 181
                                      AIDENKOKALAAALGQIEKQFGKGSIMRLGEDRSMDVKTISTGSLSLDIALGAGGLPMGR
                                                                                                                                                                                                                                                                           TGEQALEICDALARSGAVDVIVVDSVAALTPKAEIEGEIGDSHMGLAARMMSQAMRKLAG
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MEDLINE-2295/627; PubMed=14528314; DOI=10.1038/nbt886;
MEDLINE-2295/627; PubMed=14528314; DOI=10.1038/nbt886;
MEDLINE-2295/627; PubMed C., Frangeul L., Buchrieser C., Givaudan A., Taourit S., Bocs B., Borsaux-Eude C., Chandler M., Charles J.-F., Dassa E., Dercose R., Derzelle S., Freyssinet G., Gaudriault S., Medigue C., Lanois A., Powell K., Siguier P., Vincent R., Wingate V., Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;

"The genome sequence of the entomopathogenic bacterium Photorhabdus luminescens."
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-I- FUNCTION: Can catalyze the hydrolysis of ATP in the presence of single-stranded DNA, the ATP-dependent uptake of single-stranded DNA by duplex DNA, and the ATP-dependent hybridization of homologous single-stranded DNAs. It interacts with lexA causing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RecA protein (Recombinase A).
Mane=recA; OrderedLocusNames=plu1249;
Photorhabdus luminescens (subsp. laumondii).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaises;
Enterobacteriacese; Photorhabdus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
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SMR; Q7N7A6; 4-129.
PhotoList; plu1249; -.
HAMAP; MF 00268; -; 1.
Interpro; IPR001553; RecA.
Pran; PP00154; RecA; 1.
PRINTS; PR00142; RECA.
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STRAIN-SCRI 1043 / ATCC BAA-672;

PubMed=15263089; DOI=10.1073/pnas.0402424101;

PubMed=15263089; DOI=10.1073/pnas.0402424101;

PubMed=15263089; DOI=10.1073/pnas.0402424101;

PubMed=15263089; DOI=10.1073/pnas.0402424101;

Polbera M.C., Thomson N.P., Bentley S.D., Churcher L.J.C., Mungall K., Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K., Atkin R., Bason N., Atkin R., Dongett J., Christoper C., Quail M.A., Sanders M., Walker D., Whitehead S., Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S., Salmond G.P.C., Bicch P.R.J., Parkhill J., Toth I.K.;

"Genome sequence of the enterobacterial phytopathogen Erwinia carcotovora subsp. atroseptica and characterization of virulence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 TGEQALEICDALTRSGAVDVIIVDSVAALIPRAEIEGEIGDSHMGLAARMASQAMRKLAG
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Name=recA; OrderedLocusNames=ECA3369;
Brwinia carotovova (Subsp. atroseptica) (Pectobacterium atrosepticum).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pectobacterium.
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-1- FUNCTION: Can catalyze the hydrolysis of ATP in the presence of single-stranded DNA, the ATP-dependent uptake of single-stranded DNA by duplex DNA, and the ATP-dependent hybridization of homologous single-stranded DNAs. It interacts with lexA causing its activation and leading to its autocatalytic cleavage (By
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PROSITE; PS00321; RECA 1; 1.
PROSITE; PS50162; RECA 2; 1.
PROSITE; PS50163; RECA 3; 1.
ATP-binding; Complete proteome; DNA damage; DNA recombination; DNA repair; DNA-binding; Nucleotide-binding; SOS response.
NP BIND 67 74
ATP (By similarity).
SEQUENCE 355 AA; 38381 MW; FD659ACED827AEF9 CRC64;
                                                                                                                                                                                                            , Pred. No. 8.5e-95;
16; Mismatches 11.
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SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the recA family.
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10-MAY-2005 (Rel. 47, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
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                This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Name=recA; OrderedLocusNames=YPO3307, y0881, YPO379;

Yestaina pestis.

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

Enterobacteriaceae; Yersinia.
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17 A ATP (By similarity)
SEQUENCE 357 AA; 38284 MW; 48FIFFB8232E0098 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kryukov V.M., Suchkov I.Y., Sazykin I.S., Mishankin B.N.;
Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match. 91.4%; Score 1533; DB 1; Length 3 Best Local Similarity 91.3%; Pred. No. 4e-94; Matches 303; Conservative 15; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 GKANATAWLKDNPETAKEIEKKVRELLLSNPN 332
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28-FEB-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
                                                                                                                                                     EMBL; BX950851; CAG76267.1; -; Genomic_DNA.
SMR; Q6D1S8; 4-329.
                                                                                                                                                                                       HAMAN; WOLLES, T. 3.

INTERPO; IPRO01563; AAA ATPAGE.

INTERPO; IPRO01553; RECĀ.

PRINTS; PRO0142; RECĀ.

PRINTS; PRO0142; RECĀ.

PRODOM; PD000029; RECĀ; I.

PROSTR; SMO382; AAA; I.

TIGRPAMS; TIGR02012; tigrfam_recA; I.

PROSITE; PSS00162; RECĀ. 1:

PROSITE; PSS00163; RECĀ. 1:

PROSITE; PSS0163; RECĀ. 1:
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P37858;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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MEDIAINS=22137863; PubMed=12142430;
DOI=10.1128/JB1.184.16.4601-4611.2002;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
Perra N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
Petheston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner P.R.,
                              STRAIN=CO-92 / Biovar Orientalis,
MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
Parkhill J., Waren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Peltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,
"Genome sequence of Yersinla pestis, the causative agent of plague.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=91001 / Blovar Mediaevalis;
PubMed=1536893;
Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,
Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,
Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,
Yang H., Wang J., Huang P., Yang R.;
"Complete genome sequence of Yersinia pestis strain 91001, an isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DATA RES. 11:179-197(2004).

-1- FUNCTION: Can catalyze the hydrolysis of ATP in the presence of single-stranded DA, the ATP-dependent uptake of single-stranded DNA by duplex DNA, and the ATP-dependent hybridization of homologous single-stranded DNAs. It interacts with lexA causing its activation and leading to its autocatalytic cleavage.
-1- SUBGELULURA LOCATION: Cytoplasmic (By similarity).
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TIGRFAMS; TIGR02012; tigrfam_recA; 1.
PROSITE; PS00321; RECA_1; 1.
PROSITE; PS50162; RECA_2; 1.
PROSITE; PS50163; RECA_3; 1.
ATP-binding; Complete proteome; DNA damage; DNA recombination; DNA repair; DNA-binding; Nucleotide-binding; SOS response.
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ATP (By similarity)
H -> L (in Ref. 1).
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NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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EMBL; AJ414156; CAC92539.1; -; GenomIc DNA.
EMBL; AE013691; AAM84465.1; -; Genomic_DNA.
EMBL; AE017128; AAS60652.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).
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InterPro; IPR001559; AAA ATPase.
InterPro; IPR001553; RecĀ.
Pfam; PP00154; RecA; 1.
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ProDom; PD000229; RecA; 1.
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PIR, S37586, S37586.
HSSP, P03017, 2REB.
SMR, P37858; 3-328.
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RECA_ENTAG
P33037;
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X PubMed=1535888; DOI=10.1073/pnas 0404012101;
Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin V.L.,
A Simonte M., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M.,
Derbise A., Hauser L.J., Sercia E.;
Insights into the evolution of Yersinia pestis through whole-genome
T comparison with Yersinia pseudotuberculosis."

In single-stranded DNA, the ATP-dependent uptake of single-stranded
DNA by duplex DNA, and the ATP-dependent uptake of single-stranded
DNA by duplex DNA, and the ATP-dependent hybridization of
homologous single-stranded DNAs. It interacts with lexA causing
its activation and leading to its autocatalytic cleavage (By
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                                                                                 Gaps
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Yersinia.
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                                                    91.2%; Score 1530; DB 1; Length 355; 91.6%; Pred. No. 6.3e-94;
                                                                              15; Mismatches 13; Indels
294 294 N -> Y (in Ref. 1).
315 315 I -> N (in Ref. 1).
355 AA; 37755 MM; P800D2D1AD32AB81 CRC64;
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10-MAY-2005 (Rel. 47, Last sequence update)
12-SEP-2005 (Rel. 48, Last annotation update)
RecA protein (Recombinase A).
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                                                                              Matches 304; Conservative
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Q66E70;
 CONFLICT
CONFLICT
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Submitted (JAN.1993) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Can catalyze the hydrolysis of ATP in the presence of single-stranded DNA, the ATP-dependent uptake of single-stranded DNA by duplex DNA, and the ATP-dependent hybridization of homologous single-stranded DNAs. It interacts with loxA causing its activation and leading to its autocatalytic cleavage.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Pantoea.
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TIGREAMS; TIGR02012; tigrfam_recA; 1.

PROSITE; PS0312; RECA_1; 1.

PROSITE; PS50162; RECA_2; 1.

PROSITE; PS50163; RECA_3; 1.

ATP-binding; Complete proteome; DNA damage; DNA recombination; DNA repair; DNA-binding; Nucleotide-binding; SOS response.

NP BIND
67
74
ATP (BY similarity).

SEQUENCE 356 AA; 37914 MW; D1C0D90F58C8642B CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
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EMBL; BX936398; CAH20063.1; -; Genomic DNA
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                      SMR; Q66E70; 4.329.

HAMAP, MF_00268; -; 1.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR001553; RecA.
Pfam; PF00154; RecA.
PRINTS; PR00142; RECA.
ProDom; P0000229; RecA.
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                  the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
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  EMBL outstation
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                                                                                                                                                R HSSP; P03017; 2REB.

R MRX; P33037; 3-328.

R HAMAP; MF 00068; -; 1.

HAMAP; MF 00068; -; 1.

R InterPro; IPR001553; RecĀ.

R PROM142; RECA; 1.

R PRIMTS; PR00142; RECA; 1.

R SMART; SM01382; AAA; 1.

R PROSTIE; PS00321; Ligrfam_recA; 1.

R PROSTIE; PS0163; RECA_1; 1.

R PROSTIE; PS0163; RECA_2; 1.

R PROSTIE; PS0163; RECA_2; 1.

R PROSTIE; PS0163; RECA_2; 1.

R PROSTIE; PS0163; RECA_2; 1.

R PROSTIE; PS0163; RECA_2; 1.

R PROSTIE; PS0163; RECA_2; 1.

R PROSTIE; PS0163; RECA_2; 1.

R PROSTIE; PS0163; RECA_2; 1.

R PROSTIE; PS0163; RECA_2; 1.

R PROSTIE; PS0163; RECA_2; 1.

R PROSTIE; PS0163; RECA_2; 1.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Serratia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.1%; Score 1528; DB 1; Length 353; 91.8%; Pred. No. 8.5e-94; ive 16; Mismatches 11; Indel8
the Swiss Institute of Bioinformatics and the
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MEDLINE=90094239; PubMed=2152908;
Ball T.K., Wasmuth C.R., Braunagel S.C., Benedik M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 73 ATP (By similarity)
353 AA; 37767 MW; 960F1F2698CAC46B
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16-OCT-2001 (Rel. 40, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
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Matches 302; Conservative
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P17479;
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NP BIND
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                  Bacteriol. 172:342-349(1990).

Bacteriol. 172:342-349(1990).

FUNCTION: Can catalyze the hydrolysis of ATP in the presence of single-stranded blank, the ATP-dependent uptake of single-stranded DNA by duplex DNA, and the ATP-dependent hybridization of homologous single-stranded DNAs. It interacts with lexA causing its activation and leading to its autocatalytic cleavage.

SUBCELDUAL LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00321; RECA_1; 1.
PROSITE; PS0162; RECA_2; 1.
PROSITE; PS50162; RECA_2; 1.
ATP-binding; DNA damage; DNA recombination; DNA repair; DNA-binding;
"Expression of Serratia marcescens extracellular proteins requires
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide-binding; SGs response.
INIT MET 0 0 BY similarity.
MP BIND 66 73 APP (By similarity).
SEQUENCE 353 AA; 37778 MW; A97369360970F814 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, M22935; AAA26567.1; -; Genomic_DNA.
HSSP; P03017; 2REB.
SNR; P17479; 3-328.
HAMAP; MF 00268; -; 1.
InterPro; IPR001593; RecĀ.
Pfam; PF00154; RecĀ.
Pfam; PF00154; RecĀ.
PRINTS; PR00142; RECĀ.
ProDom; PD000229; RecĀ: 1.
SNART; SN00382; AAĀ; 1.
TIGRFAMS; TIGR02012; tigrfam_recĀ; 1.
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302; Conserv
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12, Appl 11, Appl 11, Appl 11, Appl 12, Appl 12, Appl 12, Appl 12, Appl 13, Appl 11, Ap

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1 AIDENKQKALAAALGQIEKQFGKGSIMRLGEDRSMDVKTISTGSLSLDIALGAGGLPMGR
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Sequence 6, Application US/08097831
Sequence 6, Application US/08097831
Sequence 6, Application US/08097831
Sequence 6, Application
Series Inversion
Septicant Camerini-Otero, Rafael D.
APPLICANT: Angov, Evangelina
TITLE OF INVENTION: Cloning and Expression of Tag recA
NUMBER OF SEQUENCES:
ADDRESSEE: KNOBBS, MARTENS, OLSON AND BEAR
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
INFER: Pacent PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER: BADABLE FORM:
MEDIUM TYPE: PLODS/MS-DOS
COMPUTER: Date Floor PC-DOS/MS-DOS
COMPUTER: LabentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,831
FILING DATE: 19930726
CLASSIFICATION NUMBER: MIHO66.001A
TELEPONMUNICATION INFORMATION:
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                       US-09-626-343-8

US-09-626-343-11

US-09-626-343-11

US-09-354-922-12

US-09-316-051-8

US-09-516-051-11

US-09-516-695B-12

US-09-516-695B-12

US-09-516-695B-12

US-09-516-695B-12

US-09-626-410-12

US-09-626-410-12

US-09-626-410-12

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linear
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STRANDEDNESS: sir
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:: /cgn2_6/ptodata/1/iaa/f_COMB.pep:*

:: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*

:: /cgn2_6/ptodata/1/iaa/PGTVS_COMB.pep:*

:: /cgn2_6/ptodata/1/iaa/PGTVS_COMB.pep:*

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US-09-626-410-7
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US-09-626-047-7
US-09-626-047-7
US-09-626-343-7
US-09-626-343-7
US-09-626-343-7
US-09-626-343-7
US-09-626-343-14
US-09-354-922-15
US-09-354-922-15
US-09-354-922-15
US-09-316-051-7
US-09-316-051-7
US-09-316-051-7
US-09-316-051-14
US-09-516-695B-15
US-09-516-695B-15
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US-09-626-410-11
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                       GenCore version (c) 1993 - 2006
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Maximum Match 100%
Listing first 45 summaries
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GENERAL INCORDATE, STEPHEN
APPLICANT: DEL CARDAYRE, STEPHEN
APPLICANT: TOBIN, MATTHEW
APPLICANT: STEMMER, WILLEM P.C.
APPLICANT: STEMMER, WILLEM P.C.
APPLICANT: MISHULLI, JEREN
APPLICANT: CASTLE, LINDA
APPLICANT: CASTLE, LINDA
APPLICANT: REBBER, CLAUS M.
APPLICANT: REBBER, CLAUS M.
APPLICANT: BASS, STEVE
TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
TITLE OF INVENTION: SCOUNCE
TITLE OF INVENTION: SCOUNCE
CURRENT APPLICATION NUMBER: US/09/626,410
CURRENT PILING DATE: 09/116,188
PRIOR PELLING DATE: 09/116,188
ETRVKVVKNKIAAPFKQAEFQILYGEGINFYGELVDLGVKEKLIEKAGAWYSYKGEKIGQ 300
                       IVEIYGPESSGKTTLTLQVLAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSQPD 120
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Pred. No. 3.8e-167;
1; Mismatches 0;
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ilarity 99.7%;
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SEQ ID NO 9
LENGTH: 358
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US-09-626-410-9
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Matches 334; Conserv
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APPLICANT: PATTEN, PHILLIP
APPLICANT: SUBRAMMIA, VENKITSWARAN
APPLICANT: SUBRAMMIA, VENKITSWARAN
APPLICANT: CASTLE, LINDA
APPLICANT: REBBER, CLAUS M.
APPLICANT: REBBER, CLAUS M.
APPLICANT: SEQUENCE RECOMBINATION
TITLE OF INVENTION: SEQUENCE RECOMBINATION
FILE REPERENCE: 02-02072008;
CURRENT APPLICATION NUMBER: US/09/626,410
CURRENT PILING DATE: 2000-07-26
PRIOR FILING DATE: 09/116,188
PRIOR FILING DATE: 07-15-1998
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SSEQ ID NO ?
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APPLICANT: TOBIN, MATTHEW
APPLICANT: STEMMER, WILLEM P.C.
APPLICANT: MESS, JON E.
APPLICANT: MINSHULL, JEREMY
APPLICANT: PATTEN, PHILLIP
APPLICANT: SUBRAMANIA, VENKITSWARN
APPLICANT: CASTLE, LINDA
APPLICANT: KREBBER, CLAUS M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/09626410 Patent No. 6287862
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ORGANISM: Escherichia coli
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Matches 334; Conservative
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GENERAL INFORMATION:
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APPLICANT: TOBIN, MATTHEW
APPLICANT: STEMMER, WILLEM P.C.
APPLICANT: STEMMER, WILLEM P.C.
APPLICANT: STEMMER, WILLEM P.C.
APPLICANT: MINSHULL, JEREMY
APPLICANT: BATTEN, PHILLIP
APPLICANT: CASTLE, LINDA
APPLICANT: CASTLE, LINDA
APPLICANT: REBBER, CLAUS M.
APPLICANT: REBBER, CLAUS M.
APPLICANT: RESPONSION: SVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
ITILE OF INVENTION: SCOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
ITILE OF INVENTION: SCOLUTION OF WHOLE CELLS AND CRANISMS BY RECURSIVE
ITILE OF INVENTION: SCOLUTION OF WHOLE CELLS AND CRANISMS BY RECURSIVE
CURRENT APPLICATION NUMBER: US/09/116,188
CURRENT APPLICATION NUMBER: US/09/116,188
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99.8%; Score 1674; DB 2;
Best Local Similarity 99.7%; Pred. No. 3.8e-167;
Matches 334; Conservative 1; Mismatches 0;
          TITLE OF INVENTION: SEQUENCE RECOMBINATION
                                                  CURRENT APPLICATION NUMBER: US/09/116,188
CURRENT FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/09116188
Patent No. 6326204
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                                                                                                                                                                                                                            LENGTH: 358
TYPE: PRT
CRGANISM: Bscherichia coli
US-09-116-188-7
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; ORGANISM: Escherichia coli
US-09-116-188-9
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GENERAL INFORMATION:
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US-09-116-188-9
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SEQ ID NO 9
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                                                                            APPLICANT: NISS, JON E.
APPLICANT: MINSHULL, JEREMY
APPLICANT: MINSHULL, JEREMY
APPLICANT: STATEN, PHILLIP
APPLICANT: STATEN, PHILLIP
APPLICANT: CASTLE, LINDA
APPLICANT: CASTLE, LINDA
APPLICANT: CASTLE, LINDA
APPLICANT: CASTLE, LINDA
APPLICANT: BASS, STEVE
TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
TITLE OF INVENTION: BOOLOTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
TITLE OF INVENTION: BOOLOTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
FILE REFERENCE: 02-020720US
CURRENT APPLICATION NUMBER: US/09/626,410
FILE REFERENCE: 07-02-1298
RIOR APPLICATION NUMBER: 09/116,188
PRIOR FILING DATE: 07-15-1998
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 14
LENGTH: 358
TYPE: PRT
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APPLICANT: SUBRAMANIA, VENKITSWARAN
APPLICANT: CASTLE, LINDA
APPLICANT: KREBBER, CLAUS M.
APPLICANT: BASS, STBVE
TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
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US-09-626-410-14
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                          TOBIN, MATTHEW
STEMMEN, WILLEM P.C.
NESS, JON E.
MINSHULL, JERENY
PATTEN, PHILLIP
SUBRAMANAN, VENKITSWARAN
CASTLE, LINDA
KREBBER, CLAUS M.
BASS, STEVE
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DEL CARDAYRE, STEPHEN
TOBIN, MATTHEW
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APPLICANT: STEMMER, WILLEM P.C.
APPLICANT: STEMMER, WILLEM P.C.
APPLICANT: MISS, JON E.
APPLICANT: MISS, JON E.
APPLICANT: PATTEN, PHILLIP
APPLICANT: CASTLE, LINDA
APPLICANT: CASTLE, LINDA
APPLICANT: REBBER, CLAUS M.
APPLICANT: REBBER, CLAUS M.
APPLICANT: REBBER, CLAUS M.
APPLICANT: BASS, STEVE
TITLE OF INVENTION: SEQUENCE RECOMBINATION
FILE REFERENCE: 02-020720US
CURRENT APPLICATION NUMBER: US/09/626,047
CURRENT PILING DATE: 2000-07-26
PRIOR FILING DATE: 07-15-1998
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Pred. No. 3.8e-167;
1; Mismatches 0;
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                                                                                                                                                      307 GKANATAWLKDNPETAKEIEKKVRELLLSNPNSTP 341
                                                                                                                                                                                                                                                                 Sequence 7, Application US/09626047; Patent No. 6335198; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                       APPLICANT: DEL CARDAYRE, STEPHEN
APPLICANT: TOBIN, MATTHEW
APPLICANT: STEMMER, WILLEM P.C.
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Best Local Similarity 99.7%;
Matches 334; Conservative 1
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
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US-09-626-047-7
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TYPE: PRT
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US-09-626-047-9
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Fatent No. 6326204

GENERAL INFORMATION:
APPLICANT: DEL CARDAYRE, STEPHEN
APPLICANT: TOBIN, MATTHEW
APPLICANT: TOBIN, WATTHEW
APPLICANT: MESS, JON E.
APPLICANT: MISSIN, WILLEM P.C.
APPLICANT: BATTEN, PHILLIP
APPLICANT: BATTEN, PHILLIP
APPLICANT: GERBER, CLAUS M.
APPLICANT: SUBRAMANIA, VEREBER
APPLICANT: CASTLE, LINDA
APPLICANT: CASTLE, LINDA
APPLICANT: REBBER, CLAUS M.
APPLICANT: REBBER, CLAUS M.
APPLICANT: BASS, STEVE
TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
TITLE OF INVENTION: BEQUENCE RECOMBINATION
FILE REPERENCE: 02-020720US
CURRENT APPLICATION NUMBER: US/09/116,188
CURRENT FILIAG DATE: 1998-07-15
NUMBER OF SEO ID NOS: 14
SOFTWARE: PATENTIN Ver. 2.0
SOFTWARE: PATENTIN Ver. 2.0
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ORGANISM: Artificial Sequence
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TITLE OF INVENTION:
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                                                                                                     APPLICANT: NESS, JON E.
APPLICANT: NESS, JON E.
APPLICANT: BATTEN, PHILLIP
APPLICANT: SUBREMANAIA, VENKITSWARAN
APPLICANT: CASTLE, LINDA
APPLICANT: KREBER, CLAUS M.
APPLICANT: KREBER, CLAUS M.
APPLICANT: KREBER, CLAUS M.
APPLICANT: SASS, STEVE
TITLE OF INVENTION: SEQUENCE RECOMBINATION
FILE REFERENCE: 02-020720US
CURRENT APPLICATION NUMBER: U$/09/626,047
CURRENT PILLING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 09/116,188
PRIOR FILING DATE: 09/116,188
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APPLICANT: SUBRAMANIA, VENKITSWARAN
APPLICANT: CASTLE, LINDA
APPLICANT: CASTLE, CLAUS M.
APPLICANT: BASS, STRVE
APPLICANT: BASS, STRVE
TITLE OF INVENTION: BVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AIDENKOKALAAALGQIEKOFGKGSIMRLGEDRSMDVKTISTGSLSLDIALGAGGLPMGR
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T: DEL CARDAYRE, WILLEM P.C.
T: STEMMER, WILLEM P.C.
T: NINSHILL, JEREMY
SUBRAMANIA, VENKITSWARAN
CASTLE, LINDA
KREBBER, CLAUS M.
BASS, STEVE
NINSHILLY
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Patent No. 6335198
GENERAL INFORMATION:
APPLICANT: DEL CARDAYE, STEPHEN
APPLICANT: TOBIN, MATTHEW
APPLICANT: STERMEN, WILLEM P.C.
APPLICANT: NESS, JON E.
APPLICANT: MINSHULL, JEREMY
Application US/09626047
6335198
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SOFTWARE: Patentin Ver. 2.0
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US-09-626-047-9
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Best Local Similarity 99.7
Matches 334; Conservative
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LENGTH: 358
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APPLICANT: NESS, JON E.
APPLICANT: NESS, JON E.
APPLICANT: PATTEN, PHILLIP
APPLICANT: STUBRAMANIA, VENKITSWARAN
APPLICANT: STUBRAMANIA, VENKITSWARAN
APPLICANT: CASTLE, LINDA
APPLICANT: CASTLE, LINDA
APPLICANT: CASTLE, LINDA
APPLICANT: BASS, STEVE
TITLE OF INVENTION: SEQUENCE RECOMBINATION
FILE REFERENCE: 02-020727US
CURRENT APPLICATION NUMBER: US/09/626,343
FILE REFERENCE: 02-020727US
CURRENT APPLICATION NUMBER: 09/116,188
PRIOR FILING DATE: 2000-07-26
SROFTWARE: PATENTIN DATE: 07-15-1998
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 7
LENGTH: 358
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Pred. No. 3.8e-167;
1; Mismatches 0;
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SEQUENCE RECOMBINATION
                   FILE REFERENCE: 02-020720US
CURRENT APPLICATION NUMBER: US/09/626,047
CURRENT FILING DATE: 2000-07-26
FRIOR APPLICATION NUMBER: 09/116,188
PRIOR FILING DATE: 07-15-1998
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 358
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 99.7
Matches 334; Conservative
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APPLICANT: NESS, JON E.
APPLICANT: NESS, JON E.
APPLICANT: NESS, JON E.
APPLICANT: MINSHULL, JEREMY
APPLICANT: PATTEN, PHILLIP
APPLICANT: SUBRAMAIA, VENKITSWARAN
APPLICANT: CASTLE, LINDA
APPLICANT: CASTLE, LINDA
APPLICANT: RERBERE, CLAUS M.
APPLICANT: RERBERE, CLAUS M.
APPLICANT: BASS, STEVE
TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
TITLE OF INVENTION: SEQUENCE RECOMBINATION
TITLE OF INVENTION: SO100NCE RECOMBINATION
FILE REFERENCE: 02-20272US
CURRENT FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: US/09/626,343
CURRENT FILING DATE: 09/116,188
PRIOR PILLING DATE: 07-15-1998
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PALENTIN VEY. 2.0
SEQ ID NO 14
LENGTH: 358
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                        TGEQALE1CDALARSGAVDV1VVDSVAALTPKAE1EGE1GDSHMGLAARWMSQAMRKLAG
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Patent No. 6352859
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APPLICANT: DEL CARDAYEE, STEPHEN
APPLICANT: TOBIN, MATTHEW
APPLICANT: STEMMER, WILLEM P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 99.7'
Matches 334; Conservative
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US-09-626-343-14
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APPLICANT: DEL CARDAYRE, STEPHEN
APPLICANT: TOBLIN, MATTHEW
APPLICANT: STEMMEN, WILLEM P.C.
APPLICANT: MISS, JON E.
APPLICANT: MISHULL, DEREMY
APPLICANT: SUBRAMANIA, VENLISMARAN
APPLICANT: SUBRAMANIA, VENKITSWARAN
APPLICANT: CASTLE, LINDA
APPLICANT: CASTLE, LINDA
APPLICANT: REBBER, CIANS M.
APPLICANT: REBBER, CIANS M.
APPLICANT: RESOURCE RECOMBINATION
TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
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Pred. No. 3.8e-167;
1; Mismatches 0;
                                                               Query Match
99.8%; Score 1674; DB 2;
Best Local Similarity 99.7%; Pred. No. 3.8e-167;
Matches 334; Conservative 1; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/626,343
CURRENT FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 09/116,188
PRIOR FILING DATE: 07-15-1998
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN Ver. 2.0
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Best Local Similarity 99.7%;
Matches 334; Conservative
; ORGANISM: Escherichia coli
US-09-626-343-7
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ORGANISM: Escherichia coli
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                                                                                                                                 Sequence 8, Application US/09354922

Sequence 8, Application US/09354922

Patent No. 637964

GENERAL INFORMATION:
APPLICANT: DEL CARDAYEE, STEPHEN
APPLICANT: STEMMER, WILLEM P.C.
APPLICANT: STEMMER, WILLEM P.C.
APPLICANT: BATTEN, PHILLIP
APPLICANT: PATTEN, PHILLIP
APPLICANT: PATTEN, PHILLIP
APPLICANT: CASTLE, LINDA M.
APPLICANT: CASTLE, LINDA M.
APPLICANT: CASTLE, LINDA M.
APPLICANT: CASTLE, LINDA M.
APPLICANT: CASTLE, LINDA M.
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APPLICANT: APPLICANT: WINGYINN
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APPLICANT: APPLICANT: WON'Y SALT'
APPLICANT: APPLICANT: WON'Y SEQUENCE
APPLICANT: APPLICATION WUMBER: US/09/354,922
CURRENT APPLICATION WUMBER: US/09/354,922
CURRENT FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 15
SEOFTWARE: Patentin Ver. 2.0
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                                GKANATAWLKDNPETAKEIEKKVRELLLSNPNSTP 335
                                                   307 GKANATAWLKONPETAKEIEKKVRELLLSNPNSTP 341
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; Sequence 10, Application US/09354922
; Patent No. 6379964
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US-09-354-922-8
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APPLICANT: DEL CARDAYRE, STEPHEN
APPLICANT: TOBIN, MATTHEW
APPLICANT: STEMMER, WILLEM P.C.
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APPLICANT: SUBRAMANIAN, VENKITESWATAN
APPLICANT: CASTLE, LINDA A.
APPLICANT: CASTLE, LINDA A.
APPLICANT: REBBER, CLAUS M.
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APPLICANT: HUISMAN, GJALT
APPLICANT: HUISMAN, GJALT
APPLICANT: WINGHIN, GJALT
APPLICANT: WINGHINO, STOUTION OF WHOLE CELLS AND ORGANISMS BY RECU
APPLICANT: AFFHOLTER, JOSEPH A.
TITLE OF INVENTION: SEQUENCE RECOMBINATION
TITLE OF INVENTION: SEQUENCE
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TITLE OF INVENTION: SEQUENCE
CURRENT FILING DATE: 1999-07-15
SOFTWARE: PALENTUR OF SEQ ID NOS: 10
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ORGANISM: Escherichia coli
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Matches 334; Conservative
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; TYPE: PRT;
; ORGANISM: Escherichia coli
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Sequence 4319, A
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Sequence 10, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 9, Appli
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Sequence 13, Appl
Sequence 11, Appl
Sequence 75948, A
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20, Appl
61049, A
                                                                                            February 16, 2006, 01:39:50 ; Search time 123 Seconds (without alignments) 1137.990 Million cell updates/sec
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Sequence 55632, 1
Sequence 78524, 1
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US-10-194-686-8

US-10-194-686-10

US-10-194-686-12

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US-10-988-943-33

US-10-282-122A-65935

US-10-282-122A-65031

US-10-282-122A-47848

US-10-282-122A-47848

US-10-282-122A-5519

US-10-282-122A-51342

US-10-156-761-10029

US-10-282-122A-53057

US-10-282-122A-51953

US-10-282-122A-51953

US-10-282-122A-51953

US-10-282-122A-61898

US-10-282-122A-61898

US-10-282-122A-61898

US-10-282-122A-61898

US-10-282-122A-61898

US-10-282-122A-61898

US-10-282-122A-61898

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US-10-282-122A-61898

US-10-282-122A-61898

US-10-282-122A-61898

US-10-282-122A-61898

US-10-282-122A-73183
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Publication No. US20040157248A1
GENERAL INFORMATION:
APPLICANT: Cox, Michael
APPLICANT: LUSECTI, Shelley
TITLE OF INVENTION: RecA Mutants
TITLE REPERRANCE: 960296.99501
CURRENT FILION NUMBER: US/10/733,782
CURRENT FILION DAOS: 5
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3:
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Pred. No. 6.5e-152;
1; Mismatches 0;
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Fublication No. US20040157248A1
GENERAL INFORMATION:
APPLICANT: Cox, Michael
APPLICANT: Lusetti, Shelley
APPLICANT: Eggler, Aimee
ITILE OF INVENTION: RecA Mutants
FILE REPERENCE: 960296.99501
CURRENT APPLICATION NUMBER: US/10/733,782
CURRENT FILING DATE: 2003-12-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.2
                                           APPLICANT: Cox, Michael
APPLICANT: Cusetti, Shelley
APPLICANT: Eggler, Aimee
TITLE OF INVENTION: RecA Mutants
FILE REPERENCE: 960296, 99501
CURRENT APPLICATION NUMBER: US/10/733,782
CURRENT FILING DATE: 2003-12-11
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 1
Sequence 1, Application US/10733782 Publication No. US20040157248A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                            99.8%;
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Best Local Similarity 99.7%;
Matches 334; Conservative
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US-10-733-782-1
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Best Local Similarity 99.7
Matches 334; Conservative
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US-10-733-782-5
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1 AIDENKQKALAAALGQIEKQFGKGSIMRLGEDRSMDVKTISTGSLSLDIALGAGGLPMGR 60

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AFFLIGANT: AU, H.

TITLE OF INVERTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PAPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-06
PRIOR PLING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2001-12-22
PRIOR PLING DATE: 2001-12-22
PRIOR PLING DATE: 2001-12-24
PRIOR PLING DATE: 2001-12-24
PRIOR PLING DATE: 2001-12-26
PRIOR PLING DATE: 2001-12-27
PRIOR PLING DATE: 2001-12-26
PRIOR PLING DATE: 2001-12-26
PRIOR PLING DATE: 2001-12-26
PRIOR PLING DATE: 2001-12-26
PRIOR PLING DATE: 2001-12-26
PRIOR PLING DATE: 2001-12-26
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121 TGEQALEICDALARSGAVDVIVVDSVAALTPKAEIEGEIGDSHMGLAARMMSQAMRKLAG
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NUMBER OF SEQ ID NOS: 78614
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APPLICANT: Zamudio, Carlos
APPLICANT: Azamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Carr, Grant
APPLICANT: Carr, Grant
APPLICANT: Foresth, R.
APPLICANT: Korsyth, R.
APPLICANT: Xu, H.
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SEQ ID NO 43319
LENGTH: 353
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; ORGANISM: Escherichia coli
US-10-282-122A-43319
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240

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ETRVKVVKNKIAAPPKQAEPQILYGEGINPYGELVDLGVKEKLIEKAGAWYSYKGEKIGQ 300
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CURRENT APPLICATION NUMBER: US/10/194,686
CURRENT PILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: US/09/354,922
PRIOR PILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO : 10
LEMACH.
                                                                               TGEQALEICDALARSGAVDVIVVDSVAALTPKAEIEGEIGDSHMGLAARMMSQAMRKLAG
                                                                                                        181 NEKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKPYASVRLDIRRIGAVKEGENVVGS
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                        67 IVELYGPESSGKTTLTLOVIAAAOREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSOPD
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APPLICANT: TOBIN, MATTHEW
APPLICANT: STEWMER, WILLEW P.C.
APPLICANT: NESS, JON E.
APPLICANT: MESS, JON E.
APPLICANT: MINSHULL, JERENY
APPLICANT: PATTEN, PHILLIP
APPLICANT: CASTLE, LINDA A.
APPLICANT: CASTLE, LINDA A.
APPLICANT: REBBER, CLAUS M.
APPLICANT: ZHANG, YING-XIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-194-686-10
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Matches 334; Conservative
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HUISMAN, GJALT
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APPLICANT: DEL CARDAYER, STEPHEN
APPLICANT: TOBIN, MATTHEM
APPLICANT: TOBIN, MATTHEM
APPLICANT: NESS, JON E.
APPLICANT: NESS, JON E.
APPLICANT: STERMER, WILLER P.C.
APPLICANT: STERMER, WILLER
APPLICANT: STERMENANIAN, VENKITESWATAN
APPLICANT: STERMENANIAN, VENKITESWATAN
APPLICANT: CASTLE, LINDA A.
APPLICANT: CASTLE, LINDA A.
APPLICANT: CASTLE, LINDA A.
APPLICANT: CASTLE, LINDA A.
APPLICANT: APFHOLTER, JOSEPH A.
APPLICANT: THING, YING
APPLICANT: YUAN, LING
APPLICANT: YUAN, LING
APPLICANT: YUAN, LING
APPLICANT: SEQUENCE RECOMBINATION
FILE REFREENCE: 02-02030105
TITLE OF INVENTION: SEQUENCE RECOMBINATION
FILE REFREENCE: 02-02030105
TITLE OF INVENTION: SEQUENCE RECOMBINATION
FILE REFREENCE: 02-02030105
TITLE OF INVENTION NUMBER: US/09/354,922
PRIOR FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATCHIN VEY: 2.0
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                   Length 353;
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                 Score 1674; DB 4;
Pred. No. 7e-152;
1; Mismatches (
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Publication No. US20030148309A1
                 99.8%;
                                   Best Local Similarity 99.7
Matches 334; Conservative
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LENGTH: 358
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US-10-194-686-12; Sequence 12, Application US/10194686
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TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
TITLE OF INVENTION: SEQUENCE RECOMBINATION
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Jeneral Information No. US2030148309A1
JENERAL INFORMATION:
JAPPLICANT: DEL CARDAYRE, STEPHEN
JAPPLICANT: TOBIN, MATTHEW
JAPPLICANT: TOBIN, MATTHEW
APPLICANT: MINSHULL, JEREMY
APPLICANT: MINSHULL, JEREMY
APPLICANT: SUBRAMANIAN, VENKITESWATAN
FLICANT: SUBRAMANIAN, VENKITESWATAN
FLICANT: CASTLE, LINDA A.
LICANT: KREBER, CLAUS M.
LICANT: KREBER, CLAUS M.
TCANT: ZHANG, YING-XIN
ANT: COX, TONY
NT: HUISWAN, GJALT
T; YUAN, LING
T; YUAN, LING
NVENTY
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CURRENT APPLICATION NUMBER: US/10/194,686
CURRENT FILING DATE: 2002-07-11
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PRIOR FILLING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity 99.79
Matches 334; Conservative
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APPLICANT: PATTEN, PHILLIP
APPLICANT: PATTEN, PHILLIP
APPLICANT: SUBRAMAIAN, PHILLIP
APPLICANT: CASTLE, LINDA A.
APPLICANT: CASTLE, LINDA A.
APPLICANT: CASTLE, CAUS M.
APPLICANT: ZHANG, YING-XIN
APPLICANT: ZHANG, YING-XIN
APPLICANT: COX, TONY
APPLICANT: HUISMAN, GJALT
APPLICANT: WINNI, LING
APPLICANT: WINNI, LING
APPLICANT: AFFHOLTER, JOSEPH A.
ITILE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
ITILE OF INVENTION: SEQUENCE RECOMBINATION
FILE REFERENCE: 02-020730US
CURRENT APPLICATION NUMBER: US/10/194,686
CURRENT APPLICATION NUMBER: US/09/354,922
PRIOR FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 15
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                                307 GKANATAWLKDNPETAKEIEKKVRELLLSNPNSTP
301 GKANATAWLKDNPETAKEIEKKVRELLLSNPNSTP
                                                                                                                                                                                               sequence 9, Application US/10194686; Publication No. US20030148309A1; GENERAL INFORMATION: APPLICANT: DEL CARDAYRE, STEPHEN
                                                                                                                                                                                                                                                                                                              TOBIN, MATTHEW
STEMMER, WILLEM P.C.
NESS, JON E.
MINSHULL, JEREMY
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APPLICANT: KREBER, CLAUS M.
APPLICANT: BASS, STEVE
APPLICANT: BASS, STEVE
APPLICANT: CANGERIAN
APPLICANT: COX, TONY
APPLICANT: HUISMAN, GJALT
APPLICANT: TONN, LING
APPLICANT: APPLICANT: BYOLUTION: BYOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
TITLE OF INVENTION: BYOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
TITLE OF INVENTION: BYOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
TITLE OF INVENTION: SEQUENCE RECOMBINATION
TITLE OF INVENTION NUMBER: US/10/194,686
CURRENT APPLICATION NUMBER: US/10/194,686
CURRENT PILING DATE: 2002-07-11
PRIOR PILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN VET: 2.0
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APPLICANT: YURN, LING
APPLICANT: APPHOLTER, JOSEPH A.
TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 358;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.7%; Score 1656; DB 4; 98.5%; Pred. No. 3.8e-150; iive 2; Mismatches 3;
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MINSHULL, JEREMY
PATTER, PHILLIP
SUBRAMANN, VENKITESWATAN
CASTLE, LINDA A.
KREBBER, CLAUS M.
BASS, STEVE
ZHANG, YING-XIN
COX, TONY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/10194686 Publication No. US20030148309A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: DEL CARDAYRE, STEPHEN
APPLICANT: TOBIN, MATTHEW
APPLICANT: STEMMER, WILLEM P.C.
       CASTLE, LINDA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 98.7
Best Local Similarity 98.5
Matches 330; Conservative
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                                    SAPELICANT: DEL CARDAYER, STEPHEN
APPLICANT: TOBIN, MATTHEW
APPLICANT: TOBIN, MATTHEW
APPLICANT: STERMER, WILLEM P.C.
APPLICANT: STERMER, WILLEM P.C.
APPLICANT: MINSHULL, JEREMY
APPLICANT: STERMER, CLAUS
APPLICANT: SUBRAMANIAN, VENKITESWATAN
APPLICANT: GASTLE, LINDA A.
APPLICANT: CASTLE, LINDA A.
APPLICANT: CASTLE, LINDA A.
APPLICANT: CASTLE, LINDA A.
APPLICANT: CASTLE, LINDA A.
APPLICANT: APPLICANT: COX, TONY
APPLICANT: APPLICANT: APPHOLITER, JOSEPH A.
TITLE OF INVENTION: SUOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
TITLE OF INVENTION: SEQUENCE RECOMBINATION
FILE REFERENCE: 02-020730US
CURRENT APPLICATION NUMBER: US/10/194,686
CURRENT APPLICATION NUMBER: US/09/354,922
PRIOR APPLICATION NUMBER: US/09/354,922
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GENERAL INFORMATION:
APPLICANT: DEL CARAPER, STEPHEN
APPLICANT: TOBIN, MATTHEW P.C.
APPLICANT: NESS, JON E.
APPLICANT: MINSHULL, JEREMY; APPLICANT: MINSHULL, JEREMY; APPLICANT: SUBRAMANIAN, VENKITESWATAN
Publication No. US20030148309A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 358
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US-10-194-686-12
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US-10-194-686-13
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Sequence 75948, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Malone, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari

APPLICANT: Carr, Grant

APPLICANT: Travick, John

APPLICANT: Travick, John

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APPLICANT: Travick, John

APPLICANT: Travick, John

APPLICANT: Su H.

TITLE REFERENCE: ELITTA.034A

CURRENT FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR PRILNG DATE: 2000-09-06

PRIOR PRILNG DATE: 2000-09-06

PRIOR PRILNG DATE: 2000-09-06
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Pred. No. 4.8e-150;
1; Mismatches 3; Indels
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; TITLE OF INVENTION: SEQUENCE RECOMBINATION
; FILE REFERENCE: 02-020730US
; CURRENT APPLICATION NUMBER: US/10/194,686
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US/09/354,922
; PRIOR FILING DATE: 1999-07-15
; SOFTWARE OF SEQ ID NOS: 15
; SOFTWARE PARENTIN Ver. 2.0
; SEQ ID NO 11
; LENGTH: 358
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 98.8%;
Matches 331; Conservative
                                                                                                                                                                                                                                      TYPE: PRT; ORGANISM: Escherichia coli
US-10-194-686-11
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US-10-282-122A-75948
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APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Syskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Tramonco, Robert
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.0349.
TITLE REFERENCE: ELITRA.0340.
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PELING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,948
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FRIOR APPLICATION NUMBER: 60/242,578
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PELING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2010-02-16
PRIOR PILING DATE: 2010-02-16
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PATENTIN VERSION 3.1
IENGTH: 353
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Gariel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT; ORGANISM: Salmonella typhi
US-10-282-122A-75948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 97.0
Matches 325; Conservative
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61 IVEIYGPESSGKTTLTLQVIAAAQREGKTCAPIDAEHALDPIYARKLGVDIDNLLCSQPD 120
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 55632
LENGTH: 352
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                                      CURRENT PELICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
PRIOR PELING DATE: 2003-02-20
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
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; Sequence 78524, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Enterobacter cloacae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Syskind, Judith
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
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Best Local Similarity 94.3*
Matches 316; Conservative
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Mano, Liangeu
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Wall, Judith
APPLICANT: APPLICANT: Janiel
APPLICANT: Zyskind, Judith
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Yamanoco, Robert
APPLICANT: Yamanoco, Robert
APPLICANT: Yamanoco, Robert
APPLICANT: Yamanoco, Robert
APPLICANT: Yamanoco, Robert
APPLICANT: Yamanoco, Robert
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 TGEQALEICDALARSGAVDVIVVDSVAALTPKAEIEGEIGDSHMGLAARMASQAMRKLAG 181
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95.9%; Score 1609; DB 4; Length 352;
Best Local Similarity 95.2%; Pred. No. 1.2e-145;
Matches 319; Conservative 9; Mismatches 7; Indels
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
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PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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US-10-282-122A-55632
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APPLICANT: Trawick, John
APPLICANT: Yamamaco, Robert
APPLICANT: Yamamaco, Robert
APPLICANT: Yamamaco, Robert
APPLICANT: Yamamaco, Robert
APPLICANT: Yamamaco, Robert
APPLICANT: Will H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT FILING DATE: 2003-02.20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,648
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PELING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-09
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Search completed: February 16, 2006, 01:44:35 Job time : 124 secs

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US-111-074-176-296
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US-110-98-686-10599
US-10-467-657-4148
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US-110-82-389-88
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US-111-082-389-124
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APPLICANT: CHIRON SpA
APPLICANT: FOUTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
ITILE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: 12003-08-11
PRIOR PLING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: Sequing9, version 1.04
SEQ ID NO 4766
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US-11-108-172-1118
US-11-079-900-1
US-10-979-821-6
US-10-979-821-6
US-10-506-443A-35
US-11-074-176-306
US-11-074-176-306
US-11-012-443-171
US-11-212-443-171
US-11-013-759-4
US-11-013-759-4
US-11-013-759-4
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US-11-1212-443-173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4766, Application US/10467657 Publication No. US20050260581A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
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Best Local Similarity 68.77
Matches 224; Conservative
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Sequence 11427, Application US/11098686

GENERAL INFORMATION:
APPLICANT: Kapur, Vivek and Gebhart, Connie J.
TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
FILE REFERENCE: 09531-128001
CURRENT APPLICATION NUMBER: US/11/098,686
CURRENT FILING DATE: 2005-04-04
PRIOR PELING DATE: 2003-10-01
PRIOR PLING DATE: 2003-10-01
PRIOR PLING DATE: 2003-10-01
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301 GKANATAWLKDNPETAKEIEKKVREL 326
                                                     NATAWLKDNPETAKEIEKKVRE 325
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NAKKYLEEHPDIYQKVQEQVRQ 325
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; ORGANISM: Lactobacillus acidophilus
US-11-074-176-296
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US-11-098-686-11427
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Sequence 10861, Application US/11098686
; Publication No. US20060024696A1
; GENREAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REPREENCE: 0933-128001,
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT PILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: PastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 11433
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11427
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US-11-098-686-10861
                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: LawBonia intracellularis
US-11-098-686-11427
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Best Local Similarity
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PRIOR FILING DATE: 2001-02-12
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Best Local S
Matches 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 TVQSLSAVTAAEVPRNPTGMGBLDRVLG-GGLVDGAVILLGGDPGIGKSTLLLQTIAKMA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 REGKTCAFIDAEHALDPIYARKIGVDID----NLLCSQPDTGEQALEICDALARSGAVDV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 IVVDSVAALTPKAEIEGEIGDSHMGLAARMMSQAMRKLAGNL----KQSNTLLIFINQIR 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197 MKIGVMFGNPETTT-----GGNALKFYASVRLDIRRIGAVKEGENVVGSETRVKVV 247
                      25 SIMRLGEDRSMDVKTISTGSLSLDIALGAGGLPMGRIVEIYGPESSGKTTLTLQVIAAAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 59; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       248 KNKIA---APFKQ------AEFQILYGEGINFYGELVDLGVKE 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNPSAIFLASYRDDTPGSCVLVTQEGSRPLLVEIQALVDDAHGFTPKRLSVGLEQ 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6; Length 459;
                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: CHIRON SpA
APPLICANT: FOUTANA Maria Rita
APPLICANT: FOUTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Blisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR PILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqMin99, version 1.04
SEQ ID NO 3092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 206, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: PONTANA Maria Rita
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATTE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
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1 Similarity 22.0%; Pred. No. 0.23;
65; Conservative 44; Mismatches 127;
                    160 EAPDLLLIDSVQTLT-SSNAEGLPGN-
                                                                                                                                                                                              Sequence 3092, Application US/10467657
Publication No. US20050260581A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Neisseria gonorrhoeae
                                                                     192 INQIRMKIGVMFG 204
                                                                                          | : | | : |
209 IGHV-TKDGTLAG 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PMGRIVEIYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPI----YARKLGVDID 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 NL------ARSGAVDVIGEQALE----ICDAL------ARSGAVDVIVVDSV 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 NIKTGNIJOSDYANMPIYVSQAKEWKFDVNCDLĹNVDELCPLAKEKKLTTGLDLLVVDHL 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 AALTPKA--EIEGEIGDSHMGLAARMMSQAMRKCAGNLKQSNTLLIFINQIRMKIGVMFG 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 PDGNLIVIAARPSMGKTVLAENIARFALKQGKAVHFQSYEMSAVELARRGMAAECNIPMQ 260
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                                                                                                                                                                                                                                                                                                                                                                     1 AIDENKOKALAAALGQ-IEKQFGKGSIMRLGEDRSMD-VK-TISTGSLSLDIALG-AGGL
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                                                                                                                                                                                                                                                                                                            78;
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                                                                                                                                                                                                                                               Length 453;
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APPLICANT: CHIRON SpA
APPLICANT: PONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
TITLE REPRENCE:
CURRENT PELICATION NUMBER: US/10/467,657
CURRENT PILING DATE: 2003-08-11
PRIOR PILING DATE: 2001-02-12
NUMBER: Seq ID NOS: 9218
SOFTWARE: Seq ID NOS: 9218
SOFTWARE: Seqwin99, version 1.04
SEQ ID NO 6400
                                                                                                                                                                                                                                         Query Match 6.5%; Score 109; DB 6; Length 45
Best Local Similarity 23.8%; Pred. No. 0.35;
Matches 66; Conservative 44; Mismatches 89; Indele
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NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SegWin99, version 1.04
SEQ ID NO 206
                                                                                                                      TYPE: PRT ORGANISM: Neisseria gonorrhoeae
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453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 RMMSQAMRKLAGNLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLDIRRI 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 QIEKQFGKGSIMRLGEDRSMDVKTISTGSLSLDIALGAGGLPMGRIVEIYGPESSGKTTL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                26;
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 6.2%; Score 104; DB 7; Length 454
Best Local Similarity 22.0%; Pred. No. 0.84;
Matches 55; Conservative 45; Mismatches 94; Indels
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APPLICANT: PONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Blisabetta
APPLICANT: MONACI Blisabetta
APPLICA DE INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REPERENCE:
                                                                 205 NPETITGGNALKFYASVR---LDIRRIGAVKEGENVV 238
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CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 3626, Application US/10467657; Publication No. US20050260581A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10599
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                                                                                                                             US-11-098-686-10599
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US-10-467-657-3626
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189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          307 KLTTGLDLLVVDHL-HIMPRAGRDEVAELGN-----ISRRLKNLAAEL---NIPVV 353
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APPLICANT: RECOGN. Markus
APPLICANT: Ecneder, Harrwig
APPLICANT: General: Harrwig
APPLICANT: General: Harrwig
APPLICANT: Calder, Oskar

APPLICANT: APPLICANT: Gregor
ITILE OF INVENTION: CORYNBEACTERIUM GENES ENCODING PROTEINS
ITILE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
TITLE OF INVENTION: CORYNBEACTER US/10/454,437
CURRENT APPLICATION NUMBER: US 60/141031
PRIOR PELLING DATE: 1999-06-23
PRIOR PELLING DATE: 1999-07-09
PRIOR PELLING DATE: 1999-07-09
PRIOR PELLING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932125.6
PRIOR APPLICATION NUMBER: DE 19932126.4
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PRIOR APPLICATION NUMBER: DE 19932126.0
PRIOR PELLING DATE: 1999-07-09
PRIOR PELLING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932226.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 SLSLDIALG-AGGLPMGRIVEIYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  354 LVAQLNR-----GNTK------QADKRPNMADIRGSGAIEQDANII 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94;
                                                                                                                                                                                                                                                                                                                                                                                          6.1%; Score 102; DB 6; Length 453; 23.7%; Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 50, Application US/10454437 Publication No. US20050277115A1 GENERAL INFORMATION:
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 3626
                                                                                                                                                                                                                                                               ; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3626
                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 23.7
Matches 69; Conservative
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161 DSHMGLAARMMSQAMRKLAGNLKQSNTLLI---FINQIRMKIGVMFGNPETTTGGNALKF 217
                                                                                                  218 YASVRLDIR-----RIGAVKEG---ENVVGS-ETRVKVVKNKIAAPFKQAEPQILYGEG 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 NLLCSQP-----DTGEQALEICDALARSGAVDVIVVDSVAALTPKAEIEGEIGDSHM- 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MayerKuckuk, Phillip
APPLICANT: MayerKuckuk, Phillip
APPLICANT: Banerjee, Debabrata
APPLICANT: Bertino, Joseph R.
TITLE OF INVENTION: Method for Modulating the Production of a Selected
TITLE OF INVENTION: Vivo
TITLE OF INVENTION: Vivo
TITLE OF INVENTION: Vivo
TITLE OF INVENTION: WHERE: US/11/213,368
CURRENT FILING DATE: 2005-08-26
PRIOR APPLICATION NUMBER: US/10/421,285
PRIOR APPLICATION NUMBER: US/02-04-22
PRIOR PLLING DATE: 2002-04-22
PRIOR PLLING DATE: 2002-04-22
PRIOR PLLING DATE: 2002-04-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.2
SEQ ID NO 14
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Publication No. US20050244935A1
GENERAL INFORMATION:
APPLICANT: Pompeius, Markus
APPLICANT: Schoder, Hartwig
APPLICANT: Schoder, Hartwig
APPLICANT: Applicant: Gregor
APPLICANT: Haberhauer, Gregor
APPLICANT: Haberhauer, Gregor
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CONVERBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62;
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Best Local Similarity 23.6%; Pred. No. 2.2;
Matches 53; Conservative 30; Mismatches
                                                                                                                                                                                                                         268 INFYGELVDLG--VKEKLIEKAGAWY 291
                                                                                                                                                                                                                                                                                                                                                    ; Sequence 14, Application US/11213368; Publication No. US20060003936A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: herpes virus
US-11-213-368-14
                                                                                                                                                                                                                                                                                                                                   US-11-213-368-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :| | :: | :: | :: | 320 AIDAASLLKPKLARGELQTIGATTLDEYRKHIEKDAALERRFQPV--QVPEPSVDLTVEI 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 IGLIREGEGVAAQVLVKLGADLPRVRQQVIQLLSGYEGGQGGSPEGGQGAPTGGDAVGAG 169
                                                                                                                                                                                                                                                                                                                              170 AAPGGR------PSSGSPGERSTSLVLDQFGRNLTQAAKDGK------LDPVVGR 212
                                                                                                                                                                                                                                                                                                                                                                            106 KLGVD------IDNLLCSQPDTGEQALEICDALARSGAVDVIVVDSVAALTPKAE 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 GLPM---GRIVEIYGPESSGKTTLTLQVIAAAQREGKTCAFID--AEHALDPIYARKLGV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 ---DIDNLLCSQPDTGEQALEICDALAR-----SGAVDVIVVDSVAALTPKAEIEGEIG 160
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                                                                                           Query Match 6.0%; Score 100; DB 6; Length 925;
Best Local Similarity 19.4%; Pred. No. 4.5;
Matches 75; Conservative 67; Mismatches 125; Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: CHIRON SpA
APPLICANT: CHIRON SpA
APPLICANT: CHIZA Maria Rita
APPLICANT: FIZA Mariagrazia
APPLICANT: BIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR APLICATION NUMBER: GB-0103424.8
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
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                                                                                                                                                                                         14 LGQIEKQFGKGS--IMRLGED----RSMDVKTIS-
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TYPE: PRT ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4148, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4148
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                                 ; UKGANISM: CUI
US-10-454-437-50
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LENGTH: 291
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us-10-733-782-3.rapbn

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ORGANISM: Neisseria gonorrhoeae
      ; ORGANISM: Nel
US-10-467-657-802
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NUMBER OF SEQ ID NOS: 446
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22.8%; Pred. No. 1.8;
tive 35; Mismatches 65; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR PILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 802
LENGTH: 471
TYPE: PRT
                                     CURRENT FILING DATE: 2005-03-16
PRIOR APPLICATION NUMBER: US 09/603024
PRIOR PELING DATE: 2000-06-23
PRIOR PELICATION NUMBER: US 60/141031
PRIOR APPLICATION NUMBER: US 60/14362
PRIOR PELING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-01
PRIOR PELICATION NUMBER: US 60/151281
PRIOR PELICATION NUMBER: US 60/151281
PRIOR PELING DATE: 1999-07-01
PRIOR PELING DATE: 1999-07-01
PRIOR PELING DATE: 1999-07-01
PRIOR PELING DATE: 1999-07-01
PRIOR PELING DATE: 1999-07-08
PRIOR PELING DATE: 1999-07-08
PRIOR PELING DATE: 1999-07-08
PRIOR PELING DATE: 1999-07-08
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PRIOR PELING DATE: 1999-07-09
PRIOR PELING DATE: 1999-07-09
PRIOR PELING DATE: 1999-07-09
PRIOR PELING DATE: 1999-07-09
                   CURRENT APPLICATION NUMBER: US/11/082,389 CURRENT FILING DATE: 2005-03-16
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Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA MAriagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Blisabetta
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US-11-082-389-88
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Matches 46; Conservative
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US-10-467-657-802
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TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads
TITLE OF INVENTION: agronomically interesting phenotypes
TITLE OF INVENTION: agronomically interesting phenotypes
FILE REFERENCE: (38-21)
CURRENT APPLICATION NUMBER: US/11/156,084
CURRENT FILING DATE: 2005-06-17
NUMBER OF SEQ ID NOS: 364
SOFTWARE: Patentin version 3.2
SEQ ID NO 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 INQIRMKIGVMFGNPETTTGGNALKFYASVRLDIRRI--GAVKEGENV-VGSETRVKVVK 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----KAGVTLRDPARFDLRGRLKHGQDVVIDVNVVIEGEVELGDNVEIGANC---VIK 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 N-KIAAPFKOAFFQILYGEGI---NFYGELVDLGVKEKLIEK--AGAWYSYKGEKIGQG- 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  314 NAKIGANSKIAPFSHLEGCEVGENNRIGPYARLRPQAKLADNVHVGNFVEIKNAAIGKGT 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 LAARMASQAM------RKLAGNIKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALK 216
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                                                                                                                                                                                                                                                                                                                                                                              137 AVDVIVVDSVAALTPKAEIEGEIGDSHMGLAARMMSQAMRKLAG-----NLKQSNTLLIF 191
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                                                                                                                                                                                     113 TLVLYGDVPLIDVETLETLLEAAGNEVGLLTDVPADPAGL--GRITR----DGSGSVTAI
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                                                                Gaps
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19.3%; Pred. No. 1.9;
tive 45; Mismatches 110; Indels
   ; Score 96; DB 6; Length 471; Pred. No. 3.7; 41; Mismatches 128; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 264, Application US/11156084 Publication No. US20060010515A1 GENERAL INFORMATION:
Query Match
Best Local Similarity 25.5%;
Matches 79; Conservative 4
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nes 58; Conservative
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